

SEQUENCE LISTING

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<120> Cone Snail Peptides

<130> 2314-249

<150> US 60/267,408

<151> 2001-02-09

<160> 638

<170> PatentIn version 3.0

<210> 1

<211> 290

<212> DNA

<213> Conus ammiralis

<220>

<221> CDS

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tgc acc cag gcc ctg gtt gaa cgt gct gga gaa aac cgc tca aag gag	96
Ser Thr Gln Ala Leu Val Glu Arg Ala Gly Glu Asn Arg Ser Lys Glu	
20 25 30	

aac atc aat ttt tta tta aaa aga aag aga gct gct gac agg ggg atg	144
Asn Ile Asn Phe Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met	
35 40 45	

tgg ggc gat tgc aaa gat ggg tta acg aca tgt ttt gcg ccc tca gag	192
Trp Gly Asp Cys Lys Asp Gly Leu Thr Thr Cys Phe Ala Pro Ser Glu	
50 55 60	

tgt tgt tct gag gat tgt gaa ggg agc tgc acg atg tgg tgatgacctc	241
Cys Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp	
65 70 75	

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<210> 2

<211> 76

<212> PRT

<213> Conus ammiralis

<400> 2

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10072503-24402

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Ile	Asn	Phe	Leu	Leu	Lys	Arg	Lys	Arg	Ala	Ala	Asp	Arg	Gly	Met	Trp		
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Gly	Asp	Cys	Lys	Asp	Gly	Leu	Thr	Thr	Cys	Phe	Ala	Pro	Ser	Glu	Cys		
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<222>	(1)..(31)																
<223>	Xaa at residues 18, 22 and 25 is Glu or gamma-carboxy-Glu; Xaa at residue 16 is Pro or hydroxy-Pro; Xaa at residues 3 and 31is Trp (D or L) or bromo-Trp (D or L)																
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	1				5					10					15		
tgc	acc	cag	gcc	ctg	cct	caa	ggc	ggc	gga	gaa	aaa	cgc	cca	agg	gag		96
Ser	Thr	Gln	Ala	Leu	Pro	Gln	Gly	Gly	Gly	Glu	Lys	Arg	Pro	Arg	Glu		
				20					25					30			
aac	atc	aga	ttt	tta	tca	aaa	aga	aag	aca	aat	gct	gag	cgt	tgg	agg		144
Asn	Ile	Arg	Phe	Leu	Ser	Lys	Arg	Lys	Thr	Asn	Ala	Glu	Arg	Trp	Arg		
			35					40					45				
gag	ggc	agt	tgc	acc	tct	tgg	tta	gcg	acg	tgt	acg	caa	gac	cag	caa		192
Glu	Gly	Ser	Cys	Thr	Ser	Trp	Leu	Ala	Thr	Cys	Thr	Gln	Asp	Gln	Gln		
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	1			5						10				15		
tcg	acc	cag	gcc	ctg	ttt	caa	gaa	aaa	cgc	aca	atg	aag	aag	atc	gat	96
Ser	Thr	Gln	Ala	Leu	Phe	Gln	Glu	Lys	Arg	Thr	Met	Lys	Lys	Ile	Asp	
				20					25					30		

ttt tta tca aag gga aag gca gat gct gag aag cag agg aag cgc aat 144
Phe Leu Ser Lys Gly Lys Ala Asp Ala Glu Lys Gln Arg Lys Arg Asn
35 40 45

tgc tcg gat gat tgg cag tat tgt gaa agt ccc agt gac tgc tgt agt 192
Cys Ser Asp Asp Trp Gln Tyr Cys Glu Ser Pro Ser Asp Cys Cys Ser
50 55 60

tgg gat tgt gat gtg gtc tgc tcg gga tgaactctga ccacaagtca 239
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<213> Conus ammiralis

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Thr Gln Ala Leu Phe Gln Glu Lys Arg Thr Met Lys Lys Ile Asp Phe
20 25 30

Leu Ser Lys Gly Lys Ala Asp Ala Glu Lys Gln Arg Lys Arg Asn Cys
35 40 45

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50 55 60

Asp Cys Asp Val Val Cys Ser Gly
65 70

<210> 9
<211> 25
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<213> Conus ammiralis

<220>
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<222> (1)..(25)
<223> Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residue 12
is Pro or hydroxy-Pro; Xaa at residues 6 and 18 is Trp (D or L) o
r bromo-Trp (D or L); Xaa at residue 8 is Tyr, 125I-Tyr, mono-iod
o-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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Asn Cys Ser Asp Asp Xaa Gln Xaa Cys Xaa Ser Xaa Ser Asp Cys Cys
1 5 10 15

Ser Xaa Asp Cys Asp Val Val Cys Ser
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<210> 10
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<212> DNA
<213> Conus ammiralis

<220>
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 1 5 10 15

tcg atc cag gcg gta aat caa gaa aaa cac caa cgg gca aag atc aac 96
 Ser Ile Gln Ala Val Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn
 20 25 30

ttg ctt tca aag aga aag cca cct gct gag cgt tgg tgg cgg tgg gga 144
 Leu Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly
 35 40 45

gga tgc atg gct tgg ttt ggg aaa tgt tgc aag gac tcg gaa tgt tgt 192
 Gly Cys Met Ala Trp Phe Gly Lys Cys Ser Lys Asp Ser Glu Cys Cys
 50 55 60

tct aat agt tgt gac ata acg cgc tgc gag tta atg cga ttc cca cca 240
 Ser Asn Ser Cys Asp Ile Thr Arg Cys Glu Leu Met Arg Phe Pro Pro
 65 70 75

gac tgg tgacatcgac actctcctgt tcagagtctt caag 280
 Asp Trp
 80

<210> 11
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 <213> Conus ammiralis

<400> 11
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 1 5 10 15

Ile Gln Ala Val Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn Leu
 20 25 30

Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly Gly
 35 40 45

Cys Met Ala Trp Phe Gly Lys Cys Ser Lys Asp Ser Glu Cys Cys Ser
 50 55 60

Asn Ser Cys Asp Ile Thr Arg Cys Glu Leu Met Arg Phe Pro Pro Asp
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 Trp

<210> 12
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 <213> Conus ammiralis

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 <222> (1)..(39)
 <223> Xaa at residues 19 and 31 is Glu or gamma-carboxy-Glu; Xaa at res
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 0 and 39 is Trp (D or L) or bromo-Trp (D or L)

<400> 12
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 1 5 10 15

Asp Ser Xaa Cys Cys Ser Asn Ser Cys Asp Ile Thr Arg Cys Xaa Leu
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<213> Conus ammiralis

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<213> Conus ammiralis

<210> 18

<211> 26
 <212> PRT
 <213> Conus ammiralis

<220>
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 <222> (1)..(26)
 <223> Xaa at residues 7 and 14 is Glu or gamma-carboxy-Glu; Xaa at residues 3 and 8 is Pro or hydroxy-Pro; Xaa at residue 18 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 18
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 1 5 10 15
 Ser Xaa Asn Cys His Asn Gly His Cys Thr
 20 25

<210> 19
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 1 5 10
 tcg acc cag gcc atg ttt caa ggt gat gga gaa aaa tcc cgg aaa gcg 96
 Ser Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser Arg Lys Ala 30
 20 25 30
 gag atc aac ttt tct aaa aca aga aat ttg gcg aga aac aag cag aaa 144
 Glu Ile Asn Phe Ser Lys Thr Arg Asn Leu Ala Arg Asn Lys Gln Lys 45
 35 40 45
 cgc tgc agt agt tgg gca aag tat tgt gaa gtt gac tcg gaa tgc tgt 192
 Arg Cys Ser Ser Trp Ala Lys Tyr Cys Glu Val Asp Ser Glu Cys Cys 60
 50 55 60
 tcc gaa cag tgt gta agg tct tac tgc gcg atg tgg tgatgacctc 238
 Ser Glu Gln Cys Val Arg Ser Tyr Cys Ala Met Trp 75
 65 70 75
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 <212> PRT
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<400> 20
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 20 25 30
 Ile Asn Phe Ser Lys Thr Arg Asn Leu Ala Arg Asn Lys Gln Lys Arg
 35 40 45

100287220400

Cys Ser Ser Trp Ala Lys Tyr Cys Glu Val Asp Ser Glu Cys Cys Ser
50 55 60

Glu Gln Cys Val Arg Ser Tyr Cys Ala Met Trp
65 70 75

<210> 21
<211> 27
<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residues 9, 13 adn.17 is Glu or gamma-carboxy-Glu; Xaa at
residue 13 is Pro or hydroxy-Pro; Xaa at residues 4 and 27 is Trp
(D or L) or bromo-Trp (D or L);

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residues 7 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo
-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 21
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1 5 10 15

Xaa Gln Cys Val Arg Ser Xaa Cys Ala Met Xaa
20 25

<210> 22
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<212> DNA
<213> Conus ammiralis

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<221> CDS
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1 5 10 15

ctg ctg ttt gcc ttg ggc aac ttt gtt gtg gtc cag tca gga cag ata 96
Leu Leu Phe Ala Leu Gly Asn Phe Val Val Val Gln Ser Gly Gln Ile
20 25 30

aca aga gat gtg gac aat gga cag ctc acg gac aac cgc cgt aac ctg 144
Thr Arg Asp Val Asp Asn Gly Gln Leu Thr Asp Asn Arg Arg Asn Leu
35 40 45

caa tcg aag tgg aag cca gtg agt ctc ttc atg tca cga cgg tct tgt 192
Gln Ser Lys Trp Lys Pro Val Ser Leu Phe Met Ser Arg Arg Ser Cys
50 55 60

aac aat tct tgc aat gag cat tcc gat tgc gaa tcc cat tgt att tgc 240
Asn Asn Ser Cys Asn Glu His Ser Asp Cys Glu Ser His Cys Ile Cys
65 70 75

acg ttt agc gga tgc aaa att att ttg ata taaacggatt gagtttgctc 290
Thr Phe Ser Gly Cys Lys Ile Ile Leu Ile
80 85

10072503.021102

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tcttttatatt ctttgtctgt tgtatttggt ttcctgtggt cataacgtac agagcccttt 410
aattaccttt actgctcttc acttaacctg ataaccggaa ggtccagtgc t 461

<210> 23
<211> 89
<212> PRT
<213> Conus ammiralis

<400> 23
Lys Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu Leu
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Leu Phe Ala Leu Gly Asn Phe Val Val Val Gln Ser Gly Gln Ile Thr
20 25 30
Arg Asp Val Asp Asn Gly Gln Leu Thr Asp Asn Arg Arg Asn Leu Gln
35 40 45
Ser Lys Trp Lys Pro Val Ser Leu Phe Met Ser Arg Arg Ser Cys Asn
50 55 60
Asn Ser Cys Asn Glu His Ser Asp Cys Glu Ser His Cys Ile Cys Thr
65 70 75 80
Phe Ser Gly Cys Lys Ile Ile Leu Ile
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<210> 24
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<212> PRT
<213> Conus ammiralis

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<223> Xaa at residues 8 and 13 is Glu or gamma-carboxy-Glu

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1 5 10 15
Ile Cys Thr Phe Ser Gly Cys Lys Ile Ile Leu Ile
20 25

<210> 25
<211> 459
<212> DNA
<213> Conus ammiralis

<220>
<221> CDS
<222> (7)..(270)

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Met His Leu Ser Leu Ala Arg Leu Ala Val Leu Met Leu Leu
1 5 10
ctg ctg ttt gcc ttg ggc aac ttt gtt gtg gtc cag tca gga cag ata 96
Leu Leu Phe Ala Leu Gly Asn Phe Val Val Val Gln Ser Gly Gln Ile
15 20 25 30

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aca aga gat gtg gac aat gga cag ctc acg gac aac cgc cgt aac ctg 144
 Thr Arg Asp Val Asp Asn Gly Gln Leu Thr Asp Asn Arg Arg Asn Leu
 35 40 45

caa tcg aag tgg aag cca gtg agt ctc ttc atg tca cga cgg tct tgt 192
 Gln Ser Lys Trp Lys Pro Val Ser Leu Phe Met Ser Arg Arg Ser Cys
 50 55 60

aac aat tct tgc aat gag cat tcc gat tgc gaa tcc cat tgt att tgc 240
 Asn Asn Ser Cys Asn Glu His Ser Asp Cys Glu Ser His Cys Ile Cys
 65 70 75

acg ttt aga gga tgc gga gct gtt aat ggt tgagtttgct cgtcaacatg 290
 Thr Phe Arg Gly Cys Gly Ala Val Asn Gly
 80 85

atgtcgcact acacactaca gctcctctct acagtgtgta catcgaccaa acgacgcac 350

ttttattttct ttgtctgttg tgtttgtttt cctgtgttca taacgtacag agccctttaa 410

ttactttttac tgctcttcac ttaacctgat aaccagaagg tccagtgt 459

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<211> 88

<212> PRT

<213> Conus ammiralis

<400> 26

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Phe Ala Leu Gly Asn Phe Val Val Val Gln Ser Gly Gln Ile Thr Arg
 20 25 30

Asp Val Asp Asn Gly Gln Leu Thr Asp Asn Arg Arg Asn Leu Gln Ser
 35 40 45

Lys Trp Lys Pro Val Ser Leu Phe Met Ser Arg Arg Ser Cys Asn Asn
 50 55 60

Ser Cys Asn Glu His Ser Asp Cys Glu Ser His Cys Ile Cys Thr Phe
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Arg Gly Cys Gly Ala Val Asn Gly
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<210> 27

<211> 27

<212> PRT

<213> Conus ammiralis

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residues 8 and 13 is Glu or gamma-carboxy-Glu

<400> 27

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 1 5 10 15

Ile Cys Thr Phe Arg Gly Cys Gly Ala Val Asn
 20 25

<210> 28

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<211> 387
 <212> DNA
 <213> Conus arenatus

<220>
 <221> CDS
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<400> 28
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 Met Lys Leu Thr Cys Val Val Ile Val Ala Val
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ctg ttc ctg acg gcc tgt caa ctc act aca gct gat gac tcc aga ggt 99
 Leu Phe Leu Thr Ala Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly
 15 20 25

acg cag aag cat ggt gcc ctg aga tcg acc acc aaa ctc tcc atg ttg 147
 Thr Gln Lys His Gly Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Leu
 30 35 40

act cgg ggc tgc acg cct cct ggt gga gtt tgt ggt tat cat ggt cac 195
 Thr Arg Gly Cys Thr Pro Pro Gly Gly Val Cys Gly Tyr His Gly His
 45 50 55

tgc tgc gat ttt tgc gat acg ttc ggc aat tta tgt gtg agt ggc 240
 Cys Cys Asp Phe Cys Asp Thr Phe Gly Asn Leu Cys Val Ser Gly
 60 65 70

tgacccggca tctgaccttt ccccttcttt tgctocacta tcctttttct gcctgagtcc 300

tccatacctg agagctgtca tgaaccactc aacacctact cttccggagg tttctgagga 360

gctgcattga aataaaagcc gcattgc 387

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 <212> PRT
 <213> Conus arenatus

<400> 29
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Gly
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Gly Cys Thr
 35 40 45

Pro Pro Gly Gly Val Cys Gly Tyr His Gly His Cys Cys Asp Phe Cys
 50 55 60

Asp Thr Phe Gly Asn Leu Cys Val Ser Gly
 65 70

<210> 30
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 <212> PRT
 <213> Conus arenatus

<220>
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 <223> Xaa at residues 4 and 5 is Pro or hydroxy-Pro; Xaa at residue 11

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1          5          10          15
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<213>	Conus arenatus

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                Met Ser Gly Leu Gly Ile Met Val Leu Thr
                1                5                10
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aag aag gcg atg caa agg gac gca atc aac gtc aga cgg aga aga tca 149
Lys Lys Ala Met Gln Arg Asp Ala Ile Asn Val Arg Arg Arg Arg Ser
30 35 40

gag gaa aag cac tgc tgc cac gta aat aat gga gta ccc tct tgt gcc 245
Glu Glu Lys His Cys Cys His Val Asn Asn Gly Val Pro Ser Cys Ala
60 65 70

caagtgtaaa cgagacatgt cagaaagtcg aaggtttgtgc gtatttgata agtattgttt 360
actgggatga acgga 375

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<400> 32
Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Val Phe
1          5          10          15
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Asp Ala Ile Asn Val Arg Arg Arg Arg Ser Leu Thr Arg Gly Val Val
35 40 45

Thr Glu Ala Cys Glu Glu Ser Cys Glu Glu Glu Glu Lys His Cys Cys
50 55 60

His Val Asn Asn Gly Val Pro Ser Cys Ala Val Ile Cys Trp Gly
65 70 75

<210> 33
<211> 32
<212> PRT
<213> Conus arenatus

<220>
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<222> (1)..(32)
<223> Xaa at residues 4, 7, 8, 11, 12, 13 and 14 is Glu or gamma-carboxy-Glu; Xaa at residue 25 is Pro or hydroxy-Pro; Xaa at residue 32 is Trp (D or L) or bromo-Trp (D or L)

<400> 33
Val Val Thr Xaa Ala Cys Xaa Xaa Ser Cys Xaa Xaa Xaa Xaa Lys His
1 5 10 15

Cys Cys His Val Asn Asn Gly Val Xaa Ser Cys Ala Val Ile Cys Xaa
20 25 30

<210> 34
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<213> Conus arenatus

<220>
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1 5 10

ctt cta ctt ctt gtg ttc atg gca acc agt cat cag gat gca gga gag 101
Leu Leu Leu Leu Val Phe Met Ala Thr Ser His Gln Asp Ala Gly Glu
15 20 25

aag cag gcg acg gaa agg gac gca atc aac atc aga tgg aga aga tca 149
Lys Gln Ala Thr Glu Arg Asp Ala Ile Asn Ile Arg Trp Arg Arg Ser
30 35 40

cgc act cgg aga ata gta act gag gcg tgc gaa gag tcc tgt gag gac 197
Arg Thr Arg Arg Ile Val Thr Glu Ala Cys Glu Glu Ser Cys Glu Asp
45 50 55

gag gaa aag cac tgc tgc cac gta aat aat gga gta ccc tct tgt gcc 245
Glu Glu Lys His Cys Cys His Val Asn Asn Gly Val Pro Ser Cys Ala
60 65 70

gtt ata tgc tgg gga tagtttctcg cacactgtct cattcattat tttatcagta 300
Val Ile Cys Trp Gly
75

caagtgtaaa cgagacatgt cagaaagtcg aaggttgtgc gtatttgata agtattgttt 360

actgggatga acgga 375

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<212> PRT
<213> Conus arenatus

10072602.02402

<400> 35
 Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Phe
 1 5 10 15
 Met Ala Thr Ser His Gln Asp Ala Gly Glu Lys Gln Ala Thr Glu Arg
 20 25 30
 Asp Ala Ile Asn Ile Arg Trp Arg Arg Ser Arg Thr Arg Arg Ile Val
 35 40 45
 Thr Glu Ala Cys Glu Glu Ser Cys Glu Asp Glu Glu Lys His Cys Cys
 50 55 60
 His Val Asn Asn Gly Val Pro Ser Cys Ala Val Ile Cys Trp Gly
 65 70 75

<210> 36
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 <212> PRT
 <213> Conus arenatus
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 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residues 4, 7, 8, 11, 13 adn 14 is Glu or gamma-carboxy-Glu;
 Xaa at residue 25 is Pro or hydroxy-Pro; Xaa at residue 32 is
 Trp (D or L) or bromo-Trp (D or L)

<400> 36
 Ile Val Thr Xaa Ala Cys Xaa Xaa Ser Cys Xaa Asp Xaa Xaa Lys His
 1 5 10 15
 Cys Cys His Val Asn Asn Gly Val Xaa Ser Cys Ala Val Ile Cys Xaa
 20 25 30

<210> 37
 <211> 374
 <212> DNA
 <213> Conus arenatus

<220>
 <221> CDS
 <222> (24)..(260)

<400> 37
 gagacgattg aacaaaattc agg atg tca gaa ctg gga atc atg gtg cta acg 53
 Met Ser Glu Leu Gly Ile Met Val Leu Thr
 1 5 10
 ctt cta ctt ctt gtg ttc ctg gta acc agt cat cag gat gca gga gag 101
 Leu Leu Leu Leu Val Phe Leu Val Thr Ser His Gln Asp Ala Gly Glu
 15 20 25
 aag cag gcg acg gaa agg gac gca atc aac atc aga tgg aga aga tca 149
 Lys Gln Ala Thr Glu Arg Asp Ala Ile Asn Ile Arg Trp Arg Arg Ser
 30 35 40
 ctc act cgg aga ata gta act gag gcg tgc gaa gag cac tgt gag gat 197
 Leu Thr Arg Arg Ile Val Thr Glu Ala Cys Glu Glu His Cys Glu Asp
 45 50 55
 gag gaa cag ttc tgc tgc ggc tta gag aat gga caa ccc ttt tgt gcc 245
 Glu Glu Gln Phe Cys Cys Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala
 60 65 70

1007366-040

aag aag gtg atg caa agg gac gca atc aac gtc aga cgg aga aga tca 149
Lys Lys Val Met Gln Arg Asp Ala Ile Asn Val Arg Arg Arg Arg Ser
30 35 40

cgc act cgg aga gta gta act ggg gcg tgc gaa gag cac tgt gag gac 197
Arg Thr Arg Arg Val Val Thr Gly Ala Cys Glu Glu His Cys Glu Asp
45 50 55

gag gaa aag cac tgc tgc ggc tta gag aat gga caa ccc ttt tgt gcc 245
Glu Glu Lys His Cys Cys Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala
60 65 70

cgt cta tgc tta gga tagttttctg tacactgtct tattcattat tttatcagta 300
Arg Leu Cys Leu Gly
75

caagtgaaaa caaagcatgt cagaaagtcg aaggttgtgc gtatttgata agtattgttt 360

actgggatga acgga 375

<210> 41
<211> 79
<212> PRT
<213> Conus arenatus

<400> 41
Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Phe
1 5 10 15

Met Ala Thr Ser His Gln Asp Ala Gly Glu Lys Lys Val Met Gln Arg
20 25 30

Asp Ala Ile Asn Val Arg Arg Arg Arg Ser Arg Thr Arg Arg Val Val
35 40 45

Thr Gly Ala Cys Glu Glu His Cys Glu Asp Glu Glu Lys His Cys Cys
50 55 60

Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala Arg Leu Cys Leu Gly
65 70 75

<210> 42
<211> 32
<212> PRT
<213> Conus arenatus

<220>
<221> PEPTIDE
<222> (1)..(31)
<223> Xaa at residues 7, 8, 11, 13, 14 and 21 is Glu or gamma-carboxy-Glu; Xaa at residue 25 is Pro or hydroxy-Pro

<400> 42
Val Val Thr Gly Ala Cys Xaa Xaa His Cys Xaa Asp Xaa Xaa Lys His
1 5 10 15

Cys Cys Gly Leu Xaa Asn Gly Gln Xaa Phe Cys Ala Arg Leu Cys Leu
20 25 30

<210> 43
<211> 219
<212> DNA
<213> Conus arenatus

10072602064102

<220>
 <221> CDS
 <222> (1)..(189)

<400> 43
 atg ggg aaa ctg aca ata ctg gtt ctt gtt gct gct gta ctg ttg tcg 48
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15
 acc cag gtc atg gtt caa ggt gac gga gat caa cct gca gct cgc aat 96
 Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Ala Arg Asn
 20 25 30
 gca gtg cca aaa gac gat aac cca gat gga gcg agt gga aag ttc atg 144
 Ala Val Pro Lys Asp Asp Asn Pro Asp Gly Ala Ser Gly Lys Phe Met
 35 40 45
 aat gtt cta cgt cgg tct gga tgt ccg tgg cat cct tgg tgt ggc 189
 Asn Val Leu Arg Arg Ser Gly Cys Pro Trp His Pro Trp Cys Gly
 50 55 60
 tgcacggaat ccacgattgc aatgacagcc 219

<210> 44
 <211> 63
 <212> PRT
 <213> Conus arenatus

<400> 44
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15
 Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Ala Arg Asn
 20 25 30
 Ala Val Pro Lys Asp Asp Asn Pro Asp Gly Ala Ser Gly Lys Phe Met
 35 40 45
 Asn Val Leu Arg Arg Ser Gly Cys Pro Trp His Pro Trp Cys Gly
 50 55 60

<210> 45
 <211> 9
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(9)
 <223> Xaa at residues 4 and 7 is Pro or hydroxy-Pro; Xaa at residues 5
 and 8 is Trp (D or L) or bromo-Trp (D or L)

<400> 45
 Ser Gly Cys Xaa Xaa His Xaa Xaa Cys
 1 5

<210> 46
 <211> 219
 <212> DNA
 <213> Conus arenatus

<220>
 <221> CDS
 <222> (1)..(189)

100755003430

<400> 46
 atg ggg aaa ctg aca ata ctg gtt ctt gtt gct gct gta ctg ttg tcg 48
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15

 acc cag gtc atg gtt caa ggt gac gga gat caa cct gca gct cgc aat 96
 Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Ala Arg Asn
 20 25 30

 gca gtg cca aaa gac gat aac cca gat gga gcg agt gga aag ttc atg 144
 Ala Val Pro Lys Asp Asp Asn Pro Asp Gly Ala Ser Gly Lys Phe Met
 35 40 45

 aat gtt cta cgt cgg tct gga tgt ccg tgg cgc cct tgg tgt ggc 189
 Asn Val Leu Arg Arg Ser Gly Cys Pro Trp Arg Pro Trp Cys Gly
 50 55 60

 tgcacggaat ccacgattgc aatgacagcc 219

 <210> 47
 <211> 63
 <212> PRT
 <213> Conus arenatus

 <400> 47
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15

 Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Ala Arg Asn
 20 25 30

 Ala Val Pro Lys Asp Asp Asn Pro Asp Gly Ala Ser Gly Lys Phe Met
 35 40 45

 Asn Val Leu Arg Arg Ser Gly Cys Pro Trp Arg Pro Trp Cys Gly
 50 55 60

 <210> 48
 <211> 10
 <212> PRT
 <213> Conus arenatus

 <220>
 <221> PEPTIDE
 <222> (1)..(10)
 <223> Xaa at residues 5 and 8 is Pro or hydroxy-Pro; Xaa at residues 6
 and 9 is Trp (D or L) or bromo-Trp (D or L)

 <400> 48
 Ala Ser Gly Cys Xaa Xaa Arg Xaa Xaa Cys
 1 5 10

 <210> 49
 <211> 219
 <212> DNA
 <213> Conus arenatus

 <220>
 <221> CDS
 <222> (1)..(189)

 <400> 49
 atg ggg aaa ctg aca ata ctg gtt ctt gtt gct gct gta ctg ttg tcg 48
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15

100725002021132

acc caq gtc atg ttt cga gat caa cct qca cgt cgt gat qca gtg cca 96

Thr Gln Val Met Phe Arg Asp Gln Pro Ala Arg Arg Asp Ala Val Pro
 20 25 30
 aga gac gat agc cca gat gga atg agt gga ggg ttc atg aat gtc cca 144
 Arg Asp Asp Ser Pro Asp Gly Met Ser Gly Gly Phe Met Asn Val Pro
 35 40 45
 cgt cgg tct gga tgt ccg tgg caa cct tgg tgt ggc tgatcggaat 190
 Arg Arg Ser Gly Cys Pro Trp Gln Pro Trp Cys Gly
 50 55 60
 ccacgattgc aatgacagcc 210
 <210> 53
 <211> 60
 <212> PRT
 <213> Conus arenatus
 <400> 53
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15
 Thr Gln Val Met Phe Arg Asp Gln Pro Ala Arg Arg Asp Ala Val Pro
 20 25 30
 Arg Asp Asp Ser Pro Asp Gly Met Ser Gly Gly Phe Met Asn Val Pro
 35 40 45
 Arg Arg Ser Gly Cys Pro Trp Gln Pro Trp Cys Gly
 50 55 60
 <210> 54
 <211> 9
 <212> PRT
 <213> Conus arenatus
 <220>
 <221> PEPTIDE
 <222> (1)..(9)
 <223> Xaa at residues 4 and 7 is Pro or hydroxy-Pro; Xaa at residues 5
 and 8 is Trp (D or L) or bromo-Trp (D or L)
 <400> 54
 Ser Gly Cys Xaa Xaa Gln Xaa Xaa Cys
 1 5
 <210> 55
 <211> 210
 <212> DNA
 <213> Conus arenatus
 <220>
 <221> CDS
 <222> (1)..(180)
 <400> 55
 atg ggg aaa ctg aca ata ctg gtt ctt gtt gct gct gta ctg ttg tcg 48
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
 1 5 10 15
 acc cag gcc atg gtt caa gat caa cct gca ggt cga gat gca gtt cca 96
 Thr Gln Ala Met Val Gln Asp Gln Pro Ala Gly Arg Asp Ala Val Pro
 20 25 30
 aga gac gat aac cca ggt gga acg agt gga aag ttc gtg aat gct caa 144

1007250200402
 2007250200402

aat ccg ggg aca atg tgc cct cct tgc agg tgc gat aat acc tgt 189
 Asn Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asp Asn Thr Cys
 50 55 60

taaccacaaaa aaaaaaaaaa aaaa 213

<210> 59
 <211> 63
 <212> PRT
 <213> Conus aurisiacus

<400> 59
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Val Asn Glu
 20 25 30

Arg Ala Pro Trp Leu Val Pro Ser Thr Ile Thr Thr Cys Cys Gly Tyr
 35 40 45

Asn Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asp Asn Thr Cys
 50 55 60

<210> 60
 <211> 30
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residues 2, 6, 17, 22 and 23 is Pro or hydroxy-Pro; Xaa at
 residue 3 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue
 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
 O-phospho-Tyr

<400> 60
 Ala Xaa Xaa Leu Val Xaa Ser Thr Ile Thr Thr Cys Cys Gly Xaa Asn
 1 5 10 15

Xaa Gly Thr Met Cys Xaa Xaa Cys Arg Cys Asp Asn Thr Cys
 20 25 30

<210> 61
 <211> 202
 <212> DNA
 <213> Conus bandanus

<220>
 <221> CDS
 <222> (1)..(183)

<400> 61
 atg cgc tgt ctc cca gtc ttg atc att ctt ctg ctg ctg act gca tct 48
 Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

gca cct ggc gtt gat gtc cta ccg aag acc gaa gat gat gtg ccc ctg 96
 Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu
 20 25 30

tca tct gtc tac gat aat aca aag agt atc cta cga gga ctt ctg gac 144
 Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp

70072667-57102

35 40 45
 aaa cgt gct tgc tgt ggc tac aag ctt tgc tca cca tgt taaccagcat 193
 Lys Arg Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys
 50 55 60

 gaaggatcc 202

 <210> 62
 <211> 61
 <212> PRT
 <213> Conus bandanus

 <400> 62
 Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
 Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu
 20 25 30
 Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp
 35 40 45
 Lys Arg Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys
 50 55 60

 <210> 63
 <211> 11
 <212> PRT
 <213> Conus bandanus
 <220>
 <221> PEPTIDE
 <222> (1)..(11)
 <223> Xaa at residue 10 is Pro or hydroxy-Pro; Xaa at residue 5 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-
 Tyr

 <400> 63
 Ala Cys Cys Gly Xaa Lys Leu Cys Ser Xaa Cys
 1 5 10

 <210> 64
 <211> 359
 <212> DNA
 <213> Conus characteristicus

 <220>
 <221> CDS
 <222> (7)..(246)

 <400> 64
 ggatcc atg aaa ctg acg tgc gtg gtg atc atc gcc gcg ctg ttc ctg 48
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Ala Leu Phe Leu
 1 5 10

 acg gcc tgt cag ctc aat aca gct gat gac tcc aga gat aag cag gag 96
 Thr Ala Cys Gln Leu Asn Thr Ala Asp Asp Ser Arg Asp Lys Gln Glu
 15 20 25 30

 tac cgt gca gtg agg ttg aga gac gga atg cgg aat ttc aaa ggt tcc 144
 Tyr Arg Ala Val Arg Leu Arg Asp Gly Met Arg Asn Phe Lys Gly Ser
 35 40 45

 aag cgc aac tgc ggg gaa caa ggt gaa ggt tgt gct act cgc cca tgc 192
 Lys Arg Asn Cys Gly Glu Gln Gly Glu Gly Cys Ala Thr Arg Pro Cys

10072562-292200

50 55 60

tgc tct ggt ctg agt tgc gtt ggc agc cgt cca gga ggc ctg tgc cag 240
 Cys Ser Gly Leu Ser Cys Val Gly Ser Arg Pro Gly Gly Leu Cys Gln
 65 70 75

tac ggc taatagtctg gcatctgata tttccctctt gcaactctacc ttcttttgcc 296
 Tyr Gly
 80

tgatgcatgt ttacttgtgt gtgggtcatga accactcagt agctacacct ccgaaggacg 356
 tgc 359

<210> 65
 <211> 80
 <212> PRT
 <213> Conus characteristicus

<400> 65
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Ala Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Asn Thr Ala Asp Asp Ser Arg Asp Lys Gln Glu Tyr Arg
 20 25 30
 Ala Val Arg Leu Arg Asp Gly Met Arg Asn Phe Lys Gly Ser Lys Arg
 35 40 45
 Asn Cys Gly Glu Gln Gly Glu Gly Cys Ala Thr Arg Pro Cys Cys Ser
 50 55 60
 Gly Leu Ser Cys Val Gly Ser Arg Pro Gly Gly Leu Cys Gln Tyr Gly
 65 70 75 80

<210> 66
 <211> 31
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residues 4 and 7 is Glu or gamma-carboxy-Glu; Xaa at residues 13 and 25 is Pro or hydroxy-Pro; Xaa at residue 31 is Tyr, 12 5I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 66
 Asn Cys Gly Xaa Gln Gly Xaa Gly Cys Ala Thr Arg Xaa Cys Cys Ser
 1 5 10 15
 Gly Leu Ser Cys Val Gly Ser Arg Xaa Gly Gly Leu Cys Gln Xaa
 20 25 30

<210> 67
 <211> 349
 <212> DNA
 <213> Conus characteristicus

<220>
 <221> CDS
 <222> (1)..(270)

<400> 67

10072602.021172

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<400> 69
Gly Cys Ser Gly Thr Cys His Arg Arg Xaa Asp Gly Lys Cys Arg Gly
1          5          10          15
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85

<210> 72
 <211> 42
 <212> PRT
 <213> Conus characteristicus

 <220>
 <221> PEPTIDE
 <222> (1)..(42)
 <223> Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residues 23
 , 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulph
 o-Tyr or O-phospho-Tyr

<400> 72
 Gly Cys Ser Gly Thr Cys His Arg Arg Xaa Asp Gly Lys Cys Arg Gly
 1 5 10 15

 Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His
 20 25 30

 His Phe Xaa Arg Gly Cys Thr Cys Thr Cys
 35 40

<210> 73
 <211> 348
 <212> DNA
 <213> Conus characteristicus

<220>
 <221> CDS
 <222> (1)..(264)

<400> 73
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc atc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
 1 5 10 15

 ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac 96
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30

 cgg aag agc ggc ttc tac ggt act ctg gca atg tct acc aga gga tgc 144
 Arg Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys
 35 40 45

 tct ggc act tgc cgt cgt cat cgg gac ggc aag tgt cgg ggt act tgc 192
 Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly Thr Cys
 50 55 60

 gac tgc tcc gga tac agc tat tgt cgc tgc ggt gac gct cac cat ttt 240
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
 65 70 75 80

 tac cga gga tgc acg tgt aca tgt taagggtgat taattcgatc ttttaactcg 294
 Tyr Arg Gly Cys Thr Cys Thr Cys
 85

 ttgaacgatt aaaaaaaaaa ttttagacga atatgttcga gaaaaaccga agac 348

<210> 74
 <211> 88
 <212> PRT
 <213> Conus characteristicus

10075603034403

<400> 74

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
1 5 10 15

Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
20 25 30

Arg Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys
35 40 45

Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly Thr Cys
50 55 60

Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
65 70 75 80

Tyr Arg Gly Cys Thr Cys Thr Cys
85

<210> 75

<211> 42

<212> PRT

<213> Conus characteristicus

<220>

<221> PEPTIDE

<222> (1)..(42)

<223> Xaa at residues 23, 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 75

Gly Cys Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly
1 5 10 15

Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His
20 25 30

His Phe Xaa Arg Gly Cys Thr Cys Thr Cys
35 40

<210> 76

<211> 349

<212> DNA

<213> Conus characteristicus

<220>

<221> CDS

<222> (1)..(264)

<400> 76

atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc atc 48
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
1 5 10 15

ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac 96
Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
20 25 30

ctg aag aga ggc ttc tac ggt act ctg gca atg tct acc aga gga tgc 144
Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys
35 40 45

tct ggc act tgc cgt cgt cat cgg gac ggc aag tgt cgg ggt act tgc 192
Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly Thr Cys
50 55 60

10072502.001

gac tgc tcc gga tac agc tat tgt cgc tgc ggt gac gct cac cat ttt 240
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
 65 70 75 80

tac cga gga tgc acg tgt aca tgt taagggttgat taattgactc ttttaactcg 294
 Tyr Arg Gly Cys Thr Cys Thr Cys
 85

ttgaacgatt aaaaaaaaaa atttttagagc aatatgttcg agaaaaaccg aagac 349

<210> 77
 <211> 88
 <212> PRT
 <213> Conus characteristicus

<400> 77
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
 1 5 10 15
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30
 Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys
 35 40 45
 Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly Thr Cys
 50 55 60
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
 65 70 75 80
 Tyr Arg Gly Cys Thr Cys Thr Cys
 85

<210> 78
 <211> 42
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(42)
 <223> Xaa at residues 23, 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 78
 Gly Cys Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly
 1 5 10 15
 Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His
 20 25 30
 His Phe Xaa Arg Gly Cys Thr Cys Thr Cys
 35 40

<210> 79
 <211> 345
 <212> DNA
 <213> Conus characteristicus

<220>
 <221> CDS
 <222> (1)..(264)

10072303 001132

gac tgc tcc gga tac agc tat tgt cgc tgc ggt gac gct cac cat ttt 240
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
 65 70 75 80

tac cga gga tgc acg tgt aca tgt taaggttgat taattgactc ttttaactcg 294
 Tyr Arg Gly Cys Thr Cys Thr Cys
 85

ttgaacgatt aaaaaaaaaa atttttagagc aatatgttcg agaaaaaccg aagac 349

<210> 77
 <211> 88
 <212> PRT
 <213> Conus characteristicus

<400> 77
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
 1 5 10 15
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30
 Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys
 35 40 45
 Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly Thr Cys
 50 55 60
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
 65 70 75 80
 Tyr Arg Gly Cys Thr Cys Thr Cys
 85

<210> 78
 <211> 42
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(42)
 <223> Xaa at residues 23, 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 78
 Gly Cys Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly
 1 5 10 15
 Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His
 20 25 30
 His Phe Xaa Arg Gly Cys Thr Cys Thr Cys
 35 40

<210> 79
 <211> 345
 <212> DNA
 <213> Conus characteristicus

<220>
 <221> CDS
 <222> (1)..(264)

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<400> 79
atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ttt ctt ttc acc 48
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Phe Leu Phe Thr
1 5 10 15

ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac 96
Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
20 25 30

ctg aag aga ggc ttc tac ggt act ctg gca atg tct tcc aga gga tgc 144
Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Ser Arg Gly Cys
35 40 45

tct ggc act tgc cat cgt cgt gag gac ggc aag tgt cgg ggt act tgc 192
Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly Thr Cys
50 55 60

gac tgc tcc gga tac agc tat tgt cgc tgc ggt gac gct cac cat ttt 240
Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
65 70 75 80

tac cga gga tgt acg tgt aca tgt taaggttgat taattgactc ttttaactcg 294
Tyr Arg Gly Cys Thr Cys Thr Cys
85

ttgaacgatt aaaaaaaaaat ttagagcaat atgttcgaga aaaccgaaga c 345

<210> 80
<211> 88
<212> PRT
<213> Conus characteristicus

<400> 80
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Phe Leu Phe Thr
1 5 10 15

Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
20 25 30

Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Ser Arg Gly Cys
35 40 45

Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly Thr Cys
50 55 60

Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
65 70 75 80

Tyr Arg Gly Cys Thr Cys Thr Cys
85

<210> 81
<211> 42
<212> PRT
<213> Conus characteristicus

<220>
<221> PEPTIDE
<222> {1}..(42)
<223> Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residues 23
, 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulph
o-Tyr or O-phospho-Tyr

<400> 81
Gly Cys Ser Gly Thr Cys His Arg Arg Xaa Asp Gly Lys Cys Arg Gly

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<220>
<221> CDS
<222> (1)..(264)
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<210> 83
<211> 88
<212> PRT
<213> Conus characteristicus
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<400>      83
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
 1          5          10          15
Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
          20          25          30
Leu Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Ala Arg Gly Cys
          35          40          45
Ser Gly Thr Cys His Arg Arg Gln Asn Gly Glu Cys Gln Gly Thr Cys
          50          55          60
Asp Cys Asp Gly His Asp His Cys Asp Cys Gly Asp Thr Leu Gly Thr
 65          70          75          80

```

Tyr Ser Gly Cys Val Cys Ile Cys
85

<210> 84

<211> 42

<212> PRT

<213> Conus characteristicus

<220>

<221> PEPTIDE

<222> (1)..(42)

<223> Xaa at residue 13 is Glu or gamma-carboxy-Glu; Xaa at residue 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 84

Gly Cys Ser Gly Thr Cys His Arg Arg Gln Asn Gly Xaa Cys Gln Gly
1 5 10 15

Thr Cys Asp Cys Asp Gly His Asp His Cys Asp Cys Gly Asp Thr Leu
20 25 30

Gly Thr Xaa Ser Gly Cys Val Cys Ile Cys
35 40

<210> 85

<211> 422

<212> DNA

<213> Conus characteristicus

<220>

<221> CDS

<222> (7)..(258)

<400> 85

gttaca atg cat ctg tca ctg gca cgc tca gct gtc ttg atg ttg ctt 48
Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu
1 5 10

ctg ctg ttt gcc ttg gac aac ttc gtt ggg gtc cag cca gga cag ata 96
Leu Leu Phe Ala Leu Asp Asn Phe Val Gly Val Gln Pro Gly Gln Ile
15 20 25 30

aca aga gat gtg gac aac cgc cgt aac cgg caa tcg cga tgg aag cca 144
Thr Arg Asp Val Asp Asn Arg Arg Asn Arg Gln Ser Arg Trp Lys Pro
35 40 45

agg agt ctc ttc aag tca ctt cat aaa cga gca tcg tgt gga ggg act 192
Arg Ser Leu Phe Lys Ser Leu His Lys Arg Ala Ser Cys Gly Gly Thr
50 55 60

tgc acg gaa agt gcc gat tgc cct tcc acg tgt agt act tgc tta cat 240
Cys Thr Glu Ser Ala Asp Cys Pro Ser Thr Cys Ser Thr Cys Leu His
65 70 75

gct caa tgc gag tca aca tgatgtcgca ctacagctct tctctacagt 288
Ala Gln Cys Glu Ser Thr
80

gtgtacatcg accgtacgac gcattctttta tttctttggc tgttttcattc gttttcttgt 348

gttcataaca tgcggagccc ttccgttacc tctactgctc tacacttaac ctgataacca 408

gaaaatccag tact 422

1073302-02103

Figure 1 consists of 12 sub-diagrams, numbered 1 to 12, arranged vertically. Each diagram shows a cross-section of a vortex structure. The diagrams illustrate the process of vortex merging and the formation of a single, larger vortex structure. The diagrams are labeled with numbers 1 through 12, indicating the sequence of the process.

<400>	88															
gttaca	atg	cat	ctg	tca	ctg	gca	cgc	tca	gct	gtt	ttg	atg	ttg	ctt		48
	Met	His	Leu	Ser	Leu	Ala	Arg	Ser	Ala	Val	Leu	Met	Leu	Leu		
	1				5					10						
ctg	ctg	ttt	gcc	ttg	gac	aac	ttc	gtt	ggg	gtc	caa	cca	gga	cag	ata	96
Leu	Leu	Phe	Ala	Leu	Asp	Asn	Phe	Val	Gly	Val	Gln	Pro	Gly	Gln	Ile	
15					20					25					30	
act	aga	gat	gtg	gac	aac	cgc	cgt	aac	ctg	caa	tcg	cga	tgg	aag	cca	144
Thr	Arg	Asp	Val	Asp	Asn	Arg	Arg	Asn	Leu	Gln	Ser	Arg	Trp	Lys	Pro	
				35					40					45		
agg	agt	ctc	ttc	aag	tca	ctt	cat	aaa	cga	gca	tcg	tgt	gga	ggg	act	192

Arg Ser Leu Phe Lys Ser Leu His Lys Arg Ala Ser Cys Gly Gly Thr
50 55 60
tgc acg gaa agt gcc gat tgc cct tcc acg tgt agt act tgc tta cat 240
Cys Thr Glu Ser Ala Asp Cys Pro Ser Thr Cys Ser Thr Cys Leu His
65 70 75
gct caa tgc gag tga aca tgatgtcgca ctacagctct tctctacagt 288
Ala Gln Cys Glu Thr
80
gtgtacatcg accgaccgta cgacgcatct tttatttctt tgtctgtttc attcgttttc 348
ttgagttcat aacatgcgga gcccttccgt tacctctact gctctacact taagctgata 408
accagaaaat ccagtact 426

<210> 89
<211> 82
<212> PRT
<213> Conus characteristicus

<400> 89
Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu Leu Leu
1 5 10 15
Phe Ala Leu Asp Asn Phe Val Gly Val Gln Pro Gly Gln Ile Thr Arg
20 25 30
Asp Val Asp Asn Arg Arg Asn Leu Gln Ser Arg Trp Lys Pro Arg Ser
35 40 45
Leu Phe Lys Ser Leu His Lys Arg Ala Ser Cys Gly Gly Thr Cys Thr
50 55 60
Glu Ser Ala Asp Cys Pro Ser Thr Cys Ser Thr Cys Leu His Ala Gln
65 70 75 80
Cys Glu

<210> 90
<211> 25
<212> PRT
<213> Conus characteristicus

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residues 8 and 25 is Glu or gamma-carboxy-Glu; Xaa at resi
due 13 is Pro or hydroxy-Pro

<400> 90
Ser Cys Gly Gly Thr Cys Thr Xaa Ser Ala Asp Cys Xaa Ser Thr Cys
1 5 10 15
Ser Thr Cys Leu His Ala Gln Cys Xaa
20 25

<210> 91
<211> 220
<212> DNA
<213> Conus circumcisis

<220>

1007250302402

<210> 94

<211> 64
 <212> PRT
 <213> Conus consors

<400> 94
 Gly Ile Phe Val Gly Val Gln Pro Glu Gln Ile Thr Arg Asp Val Asp
 1 5 10 15
 Lys Gly Tyr Ser Thr Asp Asp Gly His Asp Leu Leu Ser Leu Leu Lys
 20 25 30
 Gln Ile Ser Leu Arg Ala Cys Thr Gly Ser Cys Asn Ser Asp Ser Glu
 35 40 45
 Cys Tyr Asn Phe Cys Asp Cys Ile Gly Thr Arg Cys Glu Ala Gln Lys
 50 55 60

<210> 95
 <211> 27
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residues 11 and 24 is Glu or gamma-carboxy-Glu; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 95
 Ala Cys Thr Gly Ser Cys Asn Ser Asp Ser Xaa Cys Xaa Asn Phe Cys
 1 5 10 15
 Asp Cys Ile Gly Thr Arg Cys Xaa Ala Gln Lys
 20 25

<210> 96
 <211> 27
 <212> PRT
 <213> Conus delesstii

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residues 13 and 16 is Glu or gamma-carboxy-Glu; Xaa at residue 4 is Pro or hydroxy-Pro; Xaa at residue 25 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 96
 Ala Cys Lys Xaa Lys Asn Asn Leu Cys Ala Ile Thr Xaa Met Ala Xaa
 1 5 10 15
 Cys Cys Ser Gly Phe Cys Leu Ile Xaa Arg Cys
 20 25

<210> 97
 <211> 375
 <212> DNA
 <213> Conus distans

<220>
 <221> CDS
 <222> (24)..(260)

<400> 97

10072603:031003

gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53
 Met Ser Gly Leu Gly Ile Met Val Leu Thr
 1 5 10

ctt cta ctt ctt gtg ccc atg gca acc agt caa cag gat gga gga gag 101
 Leu Leu Leu Leu Val Pro Met Ala Thr Ser Gln Gln Asp Gly Gly Glu
 15 20 25

aag cag gcg atg caa agg gac gca atc aac gtc gca cca gga aca tca 149
 Lys Gln Ala Met Gln Arg Asp Ala Ile Asn Val Ala Pro Gly Thr Ser
 30 35 40

atc act cgg aga aat gta gat cag gag tgc att gac gcc tgt cag ctg 197
 Ile Thr Arg Arg Asn Val Asp Gln Glu Cys Ile Asp Ala Cys Gln Leu
 45 50 55

gag gac aag aat tgc tgt ggc aga aca gat gga gaa ccc aga tgt gcg 245
 Glu Asp Lys Asn Cys Cys Gly Arg Thr Asp Gly Glu Pro Arg Cys Ala
 60 65 70

aaa atc tgc ctc gga taatttctgt acgctgtctc attcattatt tcatccgtac 300
 Lys Ile Cys Leu Gly
 75

gagtgtaaac gagacctatt agaaagtcga aggttgtgcg taatttgata agcattgttt 360

gctgggacga acgga 375

<210> 98
 <211> 79
 <212> PRT
 <213> Conus distans

<400> 98
 Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Pro
 1 5 10 15

Met Ala Thr Ser Gln Gln Asp Gly Gly Glu Lys Gln Ala Met Gln Arg
 20 25 30

Asp Ala Ile Asn Val Ala Pro Gly Thr Ser Ile Thr Arg Arg Asn Val
 35 40 45

Asp Gln Glu Cys Ile Asp Ala Cys Gln Leu Glu Asp Lys Asn Cys Cys
 50 55 60

Gly Arg Thr Asp Gly Glu Pro Arg Cys Ala Lys Ile Cys Leu Gly
 65 70 75

<210> 99
 <211> 32
 <212> PRT
 <213> Conus distans

<220>
 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residues 5, 13 and 24 is Glu or gamma-carboxy-Glu; Xaa at
 residue 25 is Pro or hydroxy-Pro

<400> 99
 Asn Val Asp Gln Xaa Cys Ile Asp Ala Cys Gln Leu Xaa Asp Lys Asn
 1 5 10 15

Cys Cys Gly Arg Thr Asp Gly Xaa Xaa Arg Cys Ala Lys Ile Cys Leu

10072500-02100

20 25 30

<210> 100
 <211> 376
 <212> DNA
 <213> Conus distans

<220>
 <221> CDS
 <222> (24)..(260)

<400> 100
 gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53
 Met Ser Gly Leu Gly Ile Met Val Leu Thr
 1 5 10

ott cta ctt ctt gtg ccc atg gca acc agt caa cag gat gga gga gag 101
 Leu Leu Leu Leu Val Pro Met Ala Thr Ser Gln Gln Asp Gly Gly Glu
 15 20 25

aag cag gcg atg caa agg gac gca atc aac gtc gca cca gga aca tca 149
 Lys Gln Ala Met Gln Arg Asp Ala Ile Asn Val Ala Pro Gly Thr Ser
 30 35 40

atc act cgg aca gaa aca gat cag gag tgc att gac atc tgt aag cag 197
 Ile Thr Arg Thr Glu Thr Asp Gln Glu Cys Ile Asp Ile Cys Lys Gln
 45 50 55

gag gac aag aaa tgc tgc ggc aga tca aat gga gaa ccc aca tgt gcg 245
 Glu Asp Lys Lys Cys Cys Gly Arg Ser Asn Gly Glu Pro Thr Cys Ala
 60 65 70

aaa atc tgc ctc gga taatttctgt acgctgtctc gttcattatt tcgtcagtac 300
 Lys Ile Cys Leu Gly
 75

gagtttaaac gagacctatt agaaagtcga aggttcgtgc ttaatttgat aagcattggt 360

tgctgggatg aacgga 376

<210> 101
 <211> 79
 <212> PRT
 <213> Conus distans

<400> 101
 Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Pro
 1 5 10 15

Met Ala Thr Ser Gln Gln Asp Gly Gly Glu Lys Gln Ala Met Gln Arg
 20 25 30

Asp Ala Ile Asn Val Ala Pro Gly Thr Ser Ile Thr Arg Thr Glu Thr
 35 40 45

Asp Gln Glu Cys Ile Asp Ile Cys Lys Gln Glu Asp Lys Lys Cys Cys
 50 55 60

Gly Arg Ser Asn Gly Glu Pro Thr Cys Ala Lys Ile Cys Leu Gly
 65 70 75

<210> 102
 <211> 32
 <212> PRT
 <213> Conus distans

10072502-034402

<220>
 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residues 1, 5, 13 and 24 is Glu or gamma-carboxy-Glu; Xaa
 at residue 25 is Pro or hydroxy-Pro

<400> 102
 Xaa Thr Asp Gln Xaa Cys Ile Asp Ile Cys Lys Gln Xaa Asp Lys Lys
 1 5 10 15
 Cys Cys Gly Arg Ser Asn Gly Xaa Xaa Thr Cys Ala Lys Ile Cys Leu
 20 25 30

<210> 103
 <211> 376
 <212> DNA
 <213> Conus distans

<220>
 <221> CDS
 <222> (24)..(260)

<400> 103
 gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53
 Met Ser Gly Leu Gly Ile Met Val Leu Thr
 1 5 10
 ctt cta ctt ctt gtg ccc atg gca acc agt caa cag gat gga gga gag 101
 Leu Leu Leu Leu Val Pro Met Ala Thr Ser Gln Gln Asp Gly Gly Glu
 15 20 25
 aag cag gcg atg caa agg gac gca atc aac gtc gca cca gga aca tca 149
 Lys Gln Ala Met Gln Arg Asp Ala Ile Asn Val Ala Pro Gly Thr Ser
 30 35 40
 atc act cgg aga gaa aca gat cag gag tgc att gac acc tgt gag cag 197
 Ile Thr Arg Arg Glu Thr Asp Gln Glu Cys Ile Asp Thr Cys Glu Gln
 45 50 55
 gag gac aag aaa tgc tgc ggc aga aca aat gga gaa ccc gta tgt gcg 245
 Glu Asp Lys Lys Cys Cys Gly Arg Thr Asn Gly Glu Pro Val Cys Ala
 60 65 70
 aaa atc tgc ttc gga taatttctgt acgctgtctc attcataatt tcatcagtac 300
 Lys Ile Cys Phe Gly
 75
 gagtttaaac gagacctatt agaaagtcga aggttcgtgc ttaatttgat aagcattggt 360
 tgctgggatg aacgga 376

<210> 104
 <211> 79
 <212> PRT
 <213> Conus distans

<400> 104
 Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Pro
 1 5 10 15
 Met Ala Thr Ser Gln Gln Asp Gly Gly Glu Lys Gln Ala Met Gln Arg
 20 25 30
 Asp Ala Ile Asn Val Ala Pro Gly Thr Ser Ile Thr Arg Arg Glu Thr
 35 40 45

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<400> 107
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1          5          10          15
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Phe Thr Ser Asp Arg Ala Ser Asp Asp Arg Asn Thr Asn Asp Lys Ala
 20 25 30
 Ser Arg Leu Leu Ser His Val Val Arg Gly Cys Cys Gly Lys Tyr Pro
 35 40 45
 Asn Ala Ala Cys His Pro Cys Gly Cys Thr Val Gly Arg Pro Pro Tyr
 50 55 60
 Cys Asp Arg Pro Ser Gly Gly Gly Arg
 65 70

<210> 108
 <211> 30
 <212> PRT
 <213> Conus ermineus

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residue 7, 13, 21, 22 and 27 is Pro or hydroxy-Pro; Xaa at
 residues 6 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-
 -sulpho-Tyr or O-phospho-Tyr

<400> 108
 Gly Cys Cys Gly Lys Xaa Xaa Asn Ala Ala Cys His Xaa Cys Gly Cys
 1 5 10 15

Thr Val Gly Arg Xaa Xaa Xaa Cys Asp Arg Xaa Ser Gly Gly
 20 25 30

<210> 109
 <211> 241
 <212> DNA
 <213> Conus generalis

<220>
 <221> CDS
 <222> (1)..(210)

<400> 109
 gga tcc atg atg tct aaa ctg gga gtc ttg ttg acc atc tgt ctg gtt 48
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val
 1 5 10 15

ctg ttt ccc ctt act gct ctt cca ctg gat gga gaa caa cct gta gac 96
 Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp
 20 25 30

cga cat gcc gag cat atg cag gat gac aat tca gct gca cag aac ccc 144
 Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro
 35 40 45

tgg gtt att gcc atc aga cag tgt tgc acg ttc tgc aac ttt gga tgc 192
 Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys
 50 55 60

cag cct tgt tgc gtc ccc tgataacgtg ttgatgacca actttctcga g 241
 Gln Pro Cys Cys Val Pro
 65 70

<210> 110
 <211> 70
 <212> PRT

1007260209102

<213> *Conus generalis*

<400> 110

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp
20 25 30

Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro
35 40 45

Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys
50 55 60

Gln Pro Cys Cys Val Pro
65 70

<210> 111

<211> 16

<212> PRT

<213> *Conus generalis*

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 12 and 16 is
Pro or hydroxy-Pro

<400> 111

Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Val Xaa
1 5 10 15

<210> 112

<211> 404

<212> DNA

<213> *Conus geographus*

<220>

<221> CDS

<222> (18)..(242)

<400> 112

gcaagatcat cagcaga atg aac ctg acg tgc gtg ttg atc atc gcc gtg 50
Met Asn Leu Thr Cys Val Leu Ile Ile Ala Val
1 5 10

ctg ttt ctg acg gcc tgc cag ctc att gca gct gat gac tcc aga gat 98
Leu Phe Leu Thr Ala Cys Gln Leu Ile Ala Ala Asp Asp Ser Arg Asp
15 20 25

aac cag aag cac cgt gca gtg agg atg aga gac gca ttg aag aat ttc 146
Asn Gln Lys His Arg Ala Val Arg Met Arg Asp Ala Leu Lys Asn Phe
30 35 40

aaa gat tcc agg gcg tgc tcc ggt aga ggt tct aga tgt cct ccc caa 194
Lys Asp Ser Arg Ala Cys Ser Gly Arg Gly Ser Arg Cys Pro Pro Gln
45 50 55

tgc tgc atg ggt ttg acg tgc ggt cgt gag tat cca ccc aga tgc ggt 242

1002202-00100

Cys Cys Met Gly Leu Thr Cys Gly Arg Glu Tyr Pro Pro Arg Cys Gly
 60 65 70 75
 tgatatacgg tgaacaactg atatttcccc tctgtgctct accctctttt gcctgattca 302
 cccacacctg tgtgtggtca tgaaccactc agtacctaca cctctggtgg cttcagagga 362
 cgtatattaa aataaaacca cattgcaatg aaaaaaaaaa aa 404

<210> 113
 <211> 75
 <212> PRT
 <213> Conus geographus

<400> 113
 Met Asn Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Ala Ala Asp Asp Ser Arg Asp Asn Gln Lys His Arg
 20 25 30

Ala Val Arg Met Arg Asp Ala Leu Lys Asn Phe Lys Asp Ser Arg Ala
 35 40 45

Cys Ser Gly Arg Gly Ser Arg Cys Pro Pro Gln Cys Cys Met Gly Leu
 50 55 60

Thr Cys Gly Arg Glu Tyr Pro Pro Arg Cys Gly
 65 70 75

<210> 114
 <211> 27
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 22 is Glu or gamma-carboxy-Glu; Xaa at residues 10
 , 11, 24 and 25 is Pro or hydroxy-Pro; Xaa at residue 23 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
 yr

<400> 114
 Ala Cys Ser Gly Arg Gly Ser Arg Cys Xaa Xaa Gln Cys Cys Met Gly
 1 5 10 15

Leu Thr Cys Gly Arg Xaa Xaa Xaa Xaa Arg Cys
 20 25

<210> 115
 <211> 9
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(9)
 <223> Xaa at residue 7 is Pro or hydroxy-Pro

<400> 115
 Cys Phe Ile Arg Asn Cys Xaa Lys Gly
 1 5

<210> 116

1072602-02102

<211> 360
 <212> DNA
 <213> Conus geographus

<220>
 <221> CDS
 <222> (1)..(213)
 <400> 116

tgc tgc ccg agt agc aaa gag gat tcc ctg aac tgc att gag acc atg 48
 Cys Cys Pro Ser Ser Lys Glu Asp Ser Leu Asn Cys Ile Glu Thr Met
 1 5 10 15

gcg acc acg gcc acg tgc atg aag tcc aac aag ggg gag atc tac tcc 96
 Ala Thr Thr Ala Thr Cys Met Lys Ser Asn Lys Gly Glu Ile Tyr Ser
 20 25 30

tat gcg tgc ggc tac tgc ggc aag aag aag gag agc tgt ttc ggc gac 144
 Tyr Ala Cys Gly Tyr Cys Gly Lys Lys Lys Glu Ser Cys Phe Gly Asp
 35 40 45

aaa aag cca gtg act gac tac cag tgc cag acg cgg aac att ccc aac 192
 Lys Lys Pro Val Thr Asp Tyr Gln Cys Gln Thr Arg Asn Ile Pro Asn
 50 55 60

ccc tgc ggc ggc gct gct ctc tgaaggcacc aacagcacca acagcacgat 243
 Pro Cys Gly Gly Ala Ala Leu
 65 70

ctcctgtgtt tcgtcactgc atttatgacg tcaaaaccac gtcattgcatg atgacgacga 303

tctcggctat ggcatgtatt gaagaatgga aataaaccta gttttcagct gaaaaaa 360

<210> 117
 <211> 71
 <212> PRT
 <213> Conus geographus

<400> 117
 Cys Cys Pro Ser Ser Lys Glu Asp Ser Leu Asn Cys Ile Glu Thr Met
 1 5 10 15

Ala Thr Thr Ala Thr Cys Met Lys Ser Asn Lys Gly Glu Ile Tyr Ser
 20 25 30

Tyr Ala Cys Gly Tyr Cys Gly Lys Lys Lys Glu Ser Cys Phe Gly Asp
 35 40 45

Lys Lys Pro Val Thr Asp Tyr Gln Cys Gln Thr Arg Asn Ile Pro Asn
 50 55 60

Pro Cys Gly Gly Ala Ala Leu
 65 70

<210> 118
 <211> 71
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(71)

<223> Xaa at residues 7, 14, 29 and 43 is Glu or gamma-carboxy-Glu; Xaa at residues 3, 51, 63 and 65 is Pro or hydroxy-Pro; Xaa at residues 31, 33, 37 and 55 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

1007260-0400

<400> 118
 Cys Cys Xaa Ser Ser Lys Xaa Asp Ser Leu Asn Cys Ile Xaa Thr Met
 1 5 10 15
 Ala Thr Thr Ala Thr Cys Met Lys Ser Asn Lys Gly Xaa Ile Xaa Ser
 20 25 30
 Xaa Ala Cys Gly Xaa Cys Gly Lys Lys Lys Xaa Ser Cys Phe Gly Asp
 35 40 45
 Lys Lys Xaa Val Thr Asp Xaa Gln Cys Gln Thr Arg Asn Ile Xaa Asn
 50 55 60
 Xaa Cys Gly Gly Ala Ala Leu
 65 70

<210> 119
 <211> 769
 <212> DNA
 <213> Conus geographus

<220>
 <221> CDS
 <222> (97)..(300)

<220>
 <221> misc_feature
 <222> (1)..(769)
 <223> n is unknown

<400> 119
 cgggcgctgc attccggacg tgaaacagca tcgccagcaa gtgggcatag tgcaagacac 60
 tcagaacaat gacgcacata gtctganaaa ataacc atg ggt atg cgg atg ang 114
 Met Gly Met Arg Met Xaa
 1 5
 ttt agt gtg ttt cng cag gtt gtc ntg ggn acc act gtc gtt tcc ttc 162
 Phe Ser Val Phe Xaa Gln Val Val Xaa Gly Thr Thr Val Val Ser Phe
 10 15 20
 acn tca cgt cgt ggt cca aaa tct cgt cgc ggg gaa cct att ccg acc 210
 Xaa Ser Arg Arg Gly Pro Lys Ser Arg Arg Gly Glu Pro Ile Pro Thr
 25 30 35
 act gta atc aac tac ggg gag tgc tgt aag gat cca tcc tgt tgg gtt 258
 Thr Val Ile Asn Tyr Gly Glu Cys Cys Lys Asp Pro Ser Cys Trp Val
 40 45 50
 aag gtg aag gat ttc cag tgt cct gga gca agt cct ccc aac 300
 Lys Val Lys Asp Phe Gln Cys Pro Gly Ala Ser Pro Pro Asn
 55 60 65
 tgaaccacga catgtcgccc tctgcctgac ctgcttcacg ttccgtctct ttctgccact 360
 agaactcaac aactcgatcc aacagactcc tactttacct ccgtattctg aaactacttg 420
 gatttgattg tctttaatat ctactcacac ttgctgttat tacatcatcc aaaatttaac 480
 aagaacatga aagggtgtctg ttcaaacaaa atcaggcaat gacaangggg gaaagtctcc 540
 antctatctg aaaactgtca cctgtcactc tcttaaccag gtttanaact gantaccact 600
 anagctgttg tnccacatca ngatcagncc aatttgtann gtttcctttg caaaactttt 660

10072603-034403

<400> 122
agccttgata cagagctggg atctgctggt aatacttgaa agaacaagtg ctgtgagcct 60

tcattctctct ctgacttttag tttgggtcct ggagaaaacc ttgacgggca gt atg aaa 118
Met Lys
1

att tac ctg tgt ctt gct ttt gtt ctg ctc ctg gct tct acc ata gtt 166
Ile Tyr Leu Cys Leu Ala Phe Val Leu Leu Leu Ala Ser Thr Ile Val
5 10 15

gat tca ggg ctt ctt gat aaa att gag act ata aga aac tgg aaa cgc 214
Asp Ser Gly Leu Leu Asp Lys Ile Glu Thr Ile Arg Asn Trp Lys Arg
20 25 30

gat gac agc tat tgt gat gga tgc cta tgc acc ata tta aaa aaa gag 262
Asp Asp Ser Tyr Cys Asp Gly Cys Leu Cys Thr Ile Leu Lys Lys Glu
35 40 45 50

act tgc aca tcg act atg agc tgc agg gga aca tgc cga aaa gag tgg 310
Thr Cys Thr Ser Thr Met Ser Cys Arg Gly Thr Cys Arg Lys Glu Trp
55 60 65

cca tgt tgg gaa gaa gac tgc tac tgt act gaa atc caa ggt gga gct 358
Pro Cys Trp Glu Glu Asp Cys Tyr Cys Thr Glu Ile Gln Gly Gly Ala
70 75 80

tgc gtc aca ccc tca gaa tgc aaa cct gga gag tggtgaggat tggagtggcc 411
Cys Val Thr Pro Ser Glu Cys Lys Pro Gly Glu
85 90

agttccagca catacagcac catggtgccc tggacaatcg tctattgaat tgaatatgcc 471

tgtggcagga atctgtccta caaaataaaaa aaatcataag ttaaaaaa 519

<210> 123

<211> 93

<212> PRT

<213> Conus geographus

<400> 123

Met Lys Ile Tyr Leu Cys Leu Ala Phe Val Leu Leu Leu Ala Ser Thr
1 5 10 15

Ile Val Asp Ser Gly Leu Leu Asp Lys Ile Glu Thr Ile Arg Asn Trp
20 25 30

Lys Arg Asp Asp Ser Tyr Cys Asp Gly Cys Leu Cys Thr Ile Leu Lys
35 40 45

Lys Glu Thr Cys Thr Ser Thr Met Ser Cys Arg Gly Thr Cys Arg Lys
50 55 60

Glu Trp Pro Cys Trp Glu Glu Asp Cys Tyr Cys Thr Glu Ile Gln Gly
65 70 75 80

Gly Ala Cys Val Thr Pro Ser Glu Cys Lys Pro Gly Glu
85 90

<210> 124

<211> 60

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(60)

<223> Xaa at residues 16, 36, 37, 43, 56 and 59 is Glu or gamma-carboxy

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<210> 126

<211> 99
 <212> PRT
 <213> Conus geographus

<400> 126

Met Asn Ile Tyr Leu Cys Leu Ala Phe Leu Leu Phe Leu Pro Ser Thr
 1 5 10 15
 Ile Val Asp Ser Gly Leu Leu Asp Lys Ile Glu Thr Ile Arg Asn Trp
 20 25 30
 Arg Arg Asp Glu Ser Lys Cys Asp Arg Cys Asn Cys Ala Glu Leu Arg
 35 40 45
 Ser Ser Arg Cys Thr Gln Ala Ile Phe Cys Leu Thr Pro Glu Leu Cys
 50 55 60
 Thr Pro Ser Ile Ser Cys Pro Thr Gly Glu Cys Arg Cys Thr Lys Phe
 65 70 75 80
 His Gln Ser Arg Cys Thr Arg Phe Val Glu Cys Val Pro Asn Lys Cys
 85 90 95

Arg Asp Ala

<210> 127
 <211> 65
 <212> PRT
 <213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(65)

<223> Xaa at residues 2, 12, 28, 40 and 56 is Glu or gamma-carboxy-Glu;
 Xaa at residues 27, 32, 37 and 59 is Pro or hydroxy-Pro

<400> 127

Asp Xaa Ser Lys Cys Asp Arg Cys Asn Cys Ala Xaa Leu Arg Ser Ser
 1 5 10 15
 Arg Cys Thr Gln Ala Ile Phe Cys Leu Thr Xaa Xaa Leu Cys Thr Xaa
 20 25 30
 Ser Ile Ser Cys Xaa Thr Gly Xaa Cys Arg Cys Thr Lys Phe His Gln
 35 40 45
 Ser Arg Cys Thr Arg Phe Val Xaa Cys Val Xaa Asn Lys Cys Arg Asp
 50 55 60
 Ala
 65

<210> 128
 <211> 29
 <212> PRT
 <213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(29)

<223> Xaa at residues 9 and 23 is Glu or gamma-carboxy-Glu; Xaa at resi-
 due 28 is Pro or hydroxy-Pro; Xaa at residue 15 is Tyr, 125I-Tyr,
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 128

Lys Phe Leu Ser Gly Gly Phe Lys Xaa Ile Val Cys His Arg Xaa Cys

1 5 10 15

Ala Lys Gly Ile Ala Lys Xaa Phe Cys Asn Cys Xaa Asp
20 25

<210> 129
<211> 7
<212> PRT
<213> Conus imperialis

<220>
<221> PEPTIDE
<222> (1)..(7)
<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 6 is Trp (D or L) or bromo-Trp (D or L)

<400> 129
Xaa Cys Gly Gln Ala Xaa Cys
1 5

<210> 130
<211> 524
<212> DNA
<213> Conus imperialis

<220>
<221> CDS
<222> (7)..(285)

<400> 130
gttaaa atg cat ctg tca ctg gca agc tca gct gct ttg atg ttg ctt 48
Met His Leu Ser Leu Ala Ser Ser Ala Ala Leu Met Leu Leu
1 5 10

ctg ctt ttt gcc ttg ggc aac ttc gtt ggg gtc cag cca gga caa ata 96
Leu Leu Phe Ala Leu Gly Asn Phe Val Gly Val Gln Pro Gly Gln Ile
15 20 25 30

aga gat ctg aac aaa gga cag ctc aag gac aac cgc cgt aac ctg caa 144
Arg Asp Leu Asn Lys Gly Gln Leu Lys Asp Asn Arg Arg Asn Leu Gln
35 40 45

tcg cag agg aaa caa atg agt ctc ctc aag tca ctt cat gat cga aat 192
Ser Gln Arg Lys Gln Met Ser Leu Leu Lys Ser Leu His Asp Arg Asn
50 55 60

ggg tgt aac ggc aac acg tgt tcc aat agc ccc tgc cct aac aac tgt 240
Gly Cys Asn Gly Asn Thr Cys Ser Asn Ser Pro Cys Pro Asn Asn Cys
65 70 75

tat tgc gat act gag gac gac tgc cac cct gac agg cgt gaa cat 285
Tyr Cys Asp Thr Glu Asp Asp Cys His Pro Asp Arg Arg Glu His
80 85 90

tagagattag agagtttccct tgtcaacatg atgtcgcacc acacctctgc tctgcagtgt 345

gtacatcgac cagtcgacgc atctgttatt tctttgtctg ttggattgta catcgaccag 405

tccacgcatac tgttatttct ttgtctgttt gatttgtttt cgtgtgttca taacacacag 465

agccttttcta ttatctgtat tgcaatacac tttgcctgat aaccagaaaag tccagtgtc 524

<210> 131
<211> 93
<212> PRT

<213> Conus imperialis

<400> 131

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Met His Leu Ser Leu Ala Ser Ser Ala Ala Leu Met Leu Leu Leu Leu
1          5          10          15
Phe Ala Leu Gly Asn Phe Val Gly Val Gln Pro Gly Gln Ile Arg Asp
          20          25          30
Leu Asn Lys Gly Gln Leu Lys Asp Asn Arg Arg Asn Leu Gln Ser Gln
          35          40          45
Arg Lys Gln Met Ser Leu Leu Lys Ser Leu His Asp Arg Asn Gly Cys
          50          55          60
Asn Gly Asn Thr Cys Ser Asn Ser Pro Cys Pro Asn Asn Cys Tyr Cys
65          70          75          80
Asp Thr Glu Asp Asp Cys His Pro Asp Arg Arg Glu His
          85          90
```

<210> 132

<211> 32

<212> PRT

<213> Conus imperialis

<220>

<221> PEPTIDE

<222> (1)..(32)

<223> Xaa at residues 22 and 31 is Glu or gamma-carboxy-Glu; Xaa at residues 13, 14 and 27 is Pro or hydroxy-Pro; Xaa at residue 18 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 132

```
Asn Gly Cys Asn Gly Asn Thr Cys Ser Asn Ser Xaa Cys Xaa Asn Asn
1          5          10          15
Cys Xaa Cys Asp Thr Xaa Asp Asp Cys His Xaa Asp Arg Arg Xaa His
          20          25          30
```

<210> 133

<211> 350

<212> DNA

<213> Conus lacterculatus

<220>

<221> CDS

<222> (1)..(273)

<400> 133

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atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc      48
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
1          5          10          15
ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca cac      96
Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
          20          25          30
ccg aag aga gag ttc cat cgt att ctg cta agg cct gac aga cag tcc      144
Pro Lys Arg Glu Phe His Arg Ile Leu Leu Arg Pro Asp Arg Gln Ser
          35          40          45
gaa acg gct tgt agg tcg ctc gga agc tac caa tgt atg ggt aaa tgc      192
Glu Thr Ala Cys Arg Ser Leu Gly Ser Tyr Gln Cys Met Gly Lys Cys
          50          55          60
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caa ctc ggg gtt cat tcc tgg tgt gaa tgc att tat aac cga ggt agt 240
 Gln Leu Gly Val His Ser Trp Cys Glu Cys Ile Tyr Asn Arg Gly Ser
 65 70 75 80

cag aag tct gga tgc gcg tgt agg tgt caa aag tgattaattg actcatttaa 293
 Gln Lys Ser Gly Cys Ala Cys Arg Cys Gln Lys
 85 90

ctcgttgaac gatttaaaaa atccagagca atatgttcga gaaaaaccga agacgac 350

<210> 134
 <211> 91
 <212> PRT
 <213> Conus lacterculatus

<400> 134
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30
 Pro Lys Arg Glu Phe His Arg Ile Leu Leu Arg Pro Asp Arg Gln Ser
 35 40 45
 Glu Thr Ala Cys Arg Ser Leu Gly Ser Tyr Gln Cys Met Gly Lys Cys
 50 55 60
 Gln Leu Gly Val His Ser Trp Cys Glu Cys Ile Tyr Asn Arg Gly Ser
 65 70 75 80
 Gln Lys Ser Gly Cys Ala Cys Arg Cys Gln Lys
 85 90

<210> 135
 <211> 45
 <212> PRT
 <213> Conus lacterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(45)
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 3 and 27 is
 Glu or gamma-carboxy-Glu; Xaa at residue 25 is Trp (D or L) or br
 omo-Trp (D or L); Xaa at residues 12 and 30 is Tyr, 125I-Tyr, mon
 o-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 135
 Xaa Ser Xaa Thr Ala Cys Arg Ser Leu Gly Ser Xaa Gln Cys Met Gly
 1 5 10 15
 Lys Cys Gln Leu Gly Val His Ser Xaa Cys Xaa Cys Ile Xaa Asn Arg
 20 25 30
 Gly Ser Gln Lys Ser Gly Cys Ala Cys Arg Cys Gln Lys
 35 40 45

<210> 136
 <211> 318
 <212> DNA
 <213> Conus lividus

<220>
 <221> CDS

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$\langle 222 \rangle \quad (7) \dots (237)$

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<210> 137
<211> 77
<212> PRT
<213> Conus lividus
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<210> 138
<211> 30
<212> PRT
<213> Conus lividus
```

```

<400> 138
Ser Cys Gly His Ser Gly Ala Gly Cys Xaa Thr Arg Xaa Cys Cys Xaa
1 5 10 15
Gly Leu His Cys Ser Gly Gly Gln Ala Gly Gly Leu Cys Val

```

20 25 30

<210> 139
 <211> 312
 <212> DNA
 <213> Conus lividus

<220>
 <221> CDS
 <222> (7)..(252)

<400> 139
 ggatcc atg aaa ctg acg tgt gtg gtg atc ata tcc gtg ctg ttc ctg 48
 Met Lys Leu Thr Cys Val Val Ile Ile Ser Val Leu Phe Leu
 1 5 10

acg gcc agt gag ttc ctt aca gct gat tac tcc aga gat aag cgg cag 96
 Thr Ala Ser Glu Phe Leu Thr Ala Asp Tyr Ser Arg Asp Lys Arg Gln
 15 20 25 30

tac cgt gct gtg agg ttg aga gac gca atg cgg aat ttc aaa ggt acc 144
 Tyr Arg Ala Val Arg Leu Arg Asp Ala Met Arg Asn Phe Lys Gly Thr
 35 40 45

agg gac tgc ggg gaa tca ggt caa ggt tgc tat agt gta cgt cct tgc 192
 Arg Asp Cys Gly Glu Ser Gly Gln Gly Cys Tyr Ser Val Arg Pro Cys
 50 55 60

tgc cct ggt ctg att tgc aaa ggc acc ggt ggt gga ggc ctg tgc cgg 240
 Cys Pro Gly Leu Ile Cys Lys Gly Thr Gly Gly Gly Gly Leu Cys Arg
 65 70 75

ccc tct ggc atc tgatatctcc cctctgtgct ccaccctctt ttgcctgagt 292
 Pro Ser Gly Ile
 80

catccataacc tgtgctcgag 312

<210> 140
 <211> 82
 <212> PRT
 <213> Conus lividus

<400> 140
 Met Lys Leu Thr Cys Val Val Ile Ile Ser Val Leu Phe Leu Thr Ala
 1 5 10 15

Ser Glu Phe Leu Thr Ala Asp Tyr Ser Arg Asp Lys Arg Gln Tyr Arg
 20 25 30

Ala Val Arg Leu Arg Asp Ala Met Arg Asn Phe Lys Gly Thr Arg Asp
 35 40 45

Cys Gly Glu Ser Gly Gln Gly Cys Tyr Ser Val Arg Pro Cys Cys Pro
 50 55 60

Gly Leu Ile Cys Lys Gly Thr Gly Gly Gly Gly Leu Cys Arg Pro Ser
 65 70 75 80

Gly Ile

<210> 141
 <211> 35
 <212> PRT

<213> Conus lividus

<220>

<221> PEPTIDE

<222> (1)..(35)

<223> Xaa at residue 4 is Glu or gamma-carboxy-Glu; Xaa at residues 14, 17 and 32 is Pro or hydroxy-Pro; Xaa at residue 10 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 141

Asp Cys Gly Xaa Ser Gly Gln Gly Cys Xaa Ser Val Arg Xaa Cys Cys
1 5 10 15

Xaa Gly Leu Ile Cys Lys Gly Thr Gly Gly Gly Gly Leu Cys Arg Xaa
20 25 30

Ser Gly Ile
35

<210> 142

<211> 6

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(6)

<223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at residue 2 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 142

Val Xaa Xaa Thr His Xaa
1 5

<210> 143

<211> 6

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(6)

<223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at residue 2 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 143

Arg Xaa Lys Asn Ser Xaa
1 5

<210> 144

<211> 7

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(7)

<223> Xaa at residue 2 is Pro or hydroxy-Pro; Xaa at residue 6 is Trp (D or L) or bromo-Trp (D or L)

<400> 144

Ala Arg Xaa Lys Asn Ser Xaa
1 5

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<210> 145
 <211> 6
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(6)
 <223> Xaa at residue 3 is Pro or hydroxy-Pro; Xaa at residue 7 is Trp (D or L) or bromo-Trp (D or L)

<400> 145
 Arg Xaa Lys Asn Ser Xaa
 1 5

<210> 146
 <211> 360
 <212> DNA
 <213> Conus miles
 <220>
 <221> CDS
 <222> (7)..(270)

<400> 146
 ggatcc atg aaa ctg acg tgc gtg gtg atc gtc gcc gtg ctg ttc ctg 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10

acg gcc tgt caa ctc att act gct gcg aat tac gcc aga gat gaa cag 96
 Thr Ala Cys Gln Leu Ile Thr Ala Ala Asn Tyr Ala Arg Asp Glu Gln
 15 20 25 30

gag tac ccc gct gtg agg tcg agc gac gtg atg cag gat tcc gaa gac 144
 Glu Tyr Pro Ala Val Arg Ser Ser Asp Val Met Gln Asp Ser Glu Asp
 35 40 45

ttg acg ttg acc aag aaa tgc acg gac gat tct cag ttc tgt aac cct 192
 Leu Thr Leu Thr Lys Lys Cys Thr Asp Asp Ser Gln Phe Cys Asn Pro
 50 55 60

tcg aat cat gac tgc tgc agt ggg aag tgt atc gac gaa gga gac aac 240
 Ser Asn His Asp Cys Cys Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn
 65 70 75

ggc ata tgc gct ata gtc cct gaa aac tct taacaatgta tactgacatt 290
 Gly Ile Cys Ala Ile Val Pro Glu Asn Ser
 80 85

tccccctctg tgctccgcgcg tccgtggcct gactcgtcca tccttgggcg tggatcatgaa 350
 ccgctcgggtt 360

<210> 147
 <211> 88
 <212> PRT
 <213> Conus miles

<400> 147
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Ala Asn Tyr Ala Arg Asp Glu Gln Glu Tyr
 20 25 30

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Pro Ala Val Arg Ser Ser Asp Val Met Gln Asp Ser Glu Asp Leu Thr
 35 40 45
 Leu Thr Lys Lys Cys Thr Asp Asp Ser Gln Phe Cys Asn Pro Ser Asn
 50 55 60
 His Asp Cys Cys Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn Gly Ile
 65 70 75 80
 Cys Ala Ile Val Pro Glu Asn Ser
 85

<210> 148
 <211> 36
 <212> PRT
 <213> Conus miles
 <220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residues 23 and 34 is Glu or gamma-carboxy-Glu; Xaa at res
 idues 10 and 33 is Pro or hydroxy-Pro

<400> 148
 Cys Thr Asp Asp Ser Gln Phe Cys Asn Xaa Ser Asn His Asp Cys Cys
 1 5 10 15
 Ser Gly Lys Cys Ile Asp Xaa Gly Asp Asn Gly Ile Cys Ala Ile Val
 20 25 30
 Xaa Xaa Asn Ser
 35

<210> 149
 <211> 357
 <212> DNA
 <213> Conus miles

<220>
 <221> CDS
 <222> (7)..(270)

<400> 149
 ggatcc atg aaa ctg acg tgt gtg gtg atc gtc gcc gtg ctg ttc ctg
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
 1 5 10
 acg gcc tgt caa ctc att act gct gcg aat tac gcc aga gat gaa cag
 Thr Ala Cys Gln Leu Ile Thr Ala Ala Asn Tyr Ala Arg Asp Glu Gln
 15 20 25 30
 gag tac cct gct gtg agg tcg agc gac gtg atg cag gat tcc gaa gac
 Glu Tyr Pro Ala Val Arg Ser Ser Asp Val Met Gln Asp Ser Glu Asp
 35 40 45
 ctg acg ttg acc aag aaa tgc acg gag gat tct cag ttc tgt aac cct
 Leu Thr Leu Thr Lys Lys Cys Thr Glu Asp Ser Gln Phe Cys Asn Pro
 50 55 60
 tcg aat cat gac tgc tgc agt ggg aag tgt atc gac gaa gga gac aac
 Ser Asn His Asp Cys Cys Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn
 65 70 75
 ggc ata tgc gct ata gtc cct gaa aac tct taacaatgta tactgacatt
 Gly Ile Cys Ala Ile Val Pro Glu Asn Ser
 80 85

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tccccctctg tgctccgccg tccgtggcct gactcgcca tccttgggcg tggatcatgaa 350
ccgctcg 357

<210> 150
<211> 88
<212> PRT
<213> Conus miles

<400> 150
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15
Cys Gln Leu Ile Thr Ala Ala Asn Tyr Ala Arg Asp Glu Gln Glu Tyr
20 25 30
Pro Ala Val Arg Ser Ser Asp Val Met Gln Asp Ser Glu Asp Leu Thr
35 40 45
Leu Thr Lys Lys Cys Thr Glu Asp Ser Gln Phe Cys Asn Pro Ser Asn
50 55 60
His Asp Cys Cys Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn Gly Ile
65 70 75 80
Cys Ala Ile Val Pro Glu Asn Ser
85

<210> 151
<211> 36
<212> PRT
<213> Conus miles

<220>
<221> PEPTIDE
<222> (1)..(36)
<223> Xaa at residues 3, 23 and 34 is Glu or gamma-carboxy-Glu; Xaa at
residues 10 and 33 is Pro or hydroxy-Pro

<400> 151
Cys Thr Xaa Asp Ser Gln Phe Cys Asn Xaa Ser Asn His Asp Cys Cys
1 5 10 15
Ser Gly Lys Cys Ile Asp Xaa Gly Asp Asn Gly Ile Cys Ala Ile Val
20 25 30
Xaa Xaa Asn Ser
35

<210> 152
<211> 327
<212> DNA
<213> Conus miliaris

<220>
<221> CDS
<222> (12)..(239)

<400> 152
ggatccatga a ctg acg tgt gtg gtg atc atc gcc gtg ctg ttc ctg acg 50
Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr
1 5 10
gcc tgt caa ctc act aca gct gtg act tcc tcc aga ggt caa cag aag 98

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Ala Cys Gln Leu Thr Thr Ala Val Thr Ser Ser Arg Gly Gln Gln Lys
15 20 25

cat cgt gct ctg agg tca act gac aaa aac tcc agg atg acc aag cgt 146
His Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Arg Met Thr Lys Arg
30 35 40 45

tgc acg cct cca ggt gga ctc tgt tac cat gct tat ccc tgc tgc agc 194
Cys Thr Pro Pro Gly Gly Leu Cys Tyr His Ala Tyr Pro Cys Cys Ser
50 55 60

aag act tgc aat ctc gat acc agc caa tgt gag cct agg tgg tca 239
Lys Thr Cys Asn Leu Asp Thr Ser Gln Cys Glu Pro Arg Trp Ser
65 70 75

tgaaccactc aataccctct cctctggagg cttcagagga actacattga aataaaaccg 299

cattgcaacg aaaaaaaaaa aaaaaaaaa 327

<210> 153
<211> 76
<212> PRT
<213> Conus miliaris

<400> 153
Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala Cys Gln
1 5 10 15

Leu Thr Thr Ala Val Thr Ser Ser Arg Gly Gln Gln Lys His Arg Ala
20 25 30

Leu Arg Ser Thr Asp Lys Asn Ser Arg Met Thr Lys Arg Cys Thr Pro
35 40 45

Pro Gly Gly Leu Cys Tyr His Ala Tyr Pro Cys Cys Ser Lys Thr Cys
50 55 60

Asn Leu Asp Thr Ser Gln Cys Glu Pro Arg Trp Ser
65 70 75

<210> 154
<211> 31
<212> PRT
<213> Conus miliaris

<220>
<221> PEPTIDE
<222> (1)..(31)
<223> Xaa at residue 27 is Glu or gamma-carboxy-Glu; Xaa at residues 3,
4, 13 and 28 is Pro or hydroxy-Pro; Xaa at residue 30 is Trp (D
or L) or bromo-Trp (D or L); Xaa at residues 9 and 12 is Tyr, 125
I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 154
Cys Thr Xaa Xaa Gly Gly Leu Cys Xaa His Ala Xaa Xaa Cys Cys Ser
1 5 10 15

Lys Thr Cys Asn Leu Asp Thr Ser Gln Cys Xaa Xaa Arg Xaa Ser
20 25 30

<210> 155
<211> 193
<212> DNA
<213> Conus monachus

<220>

<221> CDS

<222> (28)..(162)

<400> 155

tgtgtgtgtg tggttctggg tccagca tct gat gtc agg aat gcc gca gtc cac 54
 Ser Asp Val Arg Asn Ala Ala Val His
 1 5

gaa aga cag aag gat ctg gtc gtt acg gcc acc acg act tgc tgt ggt 102
 Glu Arg Gln Lys Asp Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly
 10 15 20 25

tat aat ccg atg aca atg tgc cct cct tgc atg tgc act aat acc tgc 150
 Tyr Asn Pro Met Thr Met Cys Pro Pro Cys Met Cys Thr Asn Thr Cys
 30 35 40

aaa aaa agt ggc tgatgctcca ggaccctctg aaccacgacg t 193
 Lys Lys Ser Gly
 45

<210> 156

<211> 45

<212> PRT

<213> Conus monachus

<400> 156

Ser Asp Val Arg Asn Ala Ala Val His Glu Arg Gln Lys Asp Leu Val
 1 5 10 15

Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr Asn Pro Met Thr Met Cys
 20 25 30

Pro Pro Cys Met Cys Thr Asn Thr Cys Lys Lys Ser Gly
 35 40 45

<210> 157

<211> 33

<212> PRT

<213> Conus monachus

<220>

<221> PEPTIDE

<222> (1)..(33)

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 17, 22 and 2
 3 is Pro or hydroxy-Pro; Xaa at residue 15 is Tyr, 125I-Tyr, mono-
 -iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 157

Xaa Lys Asp Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Xaa Asn
 1 5 10 15

Xaa Met Thr Met Cys Xaa Xaa Cys Met Cys Thr Asn Thr Cys Lys Lys
 20 25 30

Ser

<210> 158

<211> 350

<212> DNA

<213> Conus monachus

<220>

<221> CDS

<222> (1)..(282)

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<400> 158
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15

ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca agc 96
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Ser
 20 25 30

ctg aag agc gac ttc tat cgt gct ctg aga ggg tat gac aga cag tgc 144
 Leu Lys Ser Asp Phe Tyr Arg Ala Leu Arg Gly Tyr Asp Arg Gln Cys
 35 40 45

act ctt gtc aac aat tgt gac cgg aac ggt gag cgt gcg tgt aac ggt 192
 Thr Leu Val Asn Asn Cys Asp Arg Asn Gly Glu Arg Ala Cys Asn Gly
 50 55 60

gat tgc tct tgc gag ggc cag att tgt aaa tgc ggt tat aga gtc agt 240
 Asp Cys Ser Cys Glu Gly Gln Ile Cys Lys Cys Gly Tyr Arg Val Ser
 65 70 75 80

cct ggg aag tca gga tgc gcg tgt act tgt aga aat gcc aaa 282
 Pro Gly Lys Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys
 85 90

tgaatcattt aactcgttga aagatttttt aaaaatccag agctatatgt tcgagaaaaa 342

ccgaagac 350

<210> 159
 <211> 94
 <212> PRT
 <213> Conus monachus

<400> 159
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15

Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Ser
 20 25 30

Leu Lys Ser Asp Phe Tyr Arg Ala Leu Arg Gly Tyr Asp Arg Gln Cys
 35 40 45

Thr Leu Val Asn Asn Cys Asp Arg Asn Gly Glu Arg Ala Cys Asn Gly
 50 55 60

Asp Cys Ser Cys Glu Gly Gln Ile Cys Lys Cys Gly Tyr Arg Val Ser
 65 70 75 80

Pro Gly Lys Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys
 85 90

<210> 160
 <211> 48
 <212> PRT
 <213> Conus monachus

<220>
 <221> PEPTIDE
 <222> (1)..(48)
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 13 and 23 is
 Glu or gamma-carboxy-Glu; Xaa at residue 35 is Pro or hydroxy-Pr
 o; Xaa at residue 31 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr
 , O-sulpho-Tyr or O-phospho-Tyr

<223> Xaa at residue 11 is Pro or hydroxy-Pro

<400> 163

Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Xaa Cys Arg
1 5 10

<210> 164

<211> 450

<212> DNA

<213> Conus pennaceus

<220>

<221> CDS

<222> (1)..(234)

<400> 164

atg ttg ctt ctg ctg ttt gcc ttg ggc agc ttc gtt gtg gtc cag tca 48
Met Leu Leu Leu Leu Phe Ala Leu Gly Ser Phe Val Val Val Gln Ser
1 5 10 15

gga cag ata aca aga gat gtg gac aat ggg cag ctc gcg gac aac cgc 96
Gly Gln Ile Thr Arg Asp Val Asp Asn Gly Gln Leu Ala Asp Asn Arg
20 25 30

cgt acc ctg cga tcg cag tgg aag caa gtg agt ttc ttc aag tca ctt 144
Arg Thr Leu Arg Ser Gln Trp Lys Gln Val Ser Phe Phe Lys Ser Leu
35 40 45

gat aaa cga ctg act tgt aac gat cct tgc cag atg cat tcc gat tgc 192
Asp Lys Arg Leu Thr Cys Asn Asp Pro Cys Gln Met His Ser Asp Cys
50 55 60

ggc ata tgt gaa tgc gtg gaa aat aaa tgc ata ttt ttc atg 234
Gly Ile Cys Glu Cys Val Glu Asn Lys Cys Ile Phe Phe Met
65 70 75

taaacggatt gagtttgctt gtcaacacaa tgtcgcactg cagctcttct ctaccggtgg 294

gtacatcgac caaacgacgc atctttttatt tctttgtctg tttcgtttgt tctcctgtgt 354

tcataacgta cagagccctt taactaccct tactgtctctt cacttaacct gataacctga 414

aggtccggtg cagctggcgt agccttcaca gtttcg 450

<210> 165

<211> 78

<212> PRT

<213> Conus pennaceus

<400> 165

Met Leu Leu Leu Leu Phe Ala Leu Gly Ser Phe Val Val Val Gln Ser
1 5 10 15

Gly Gln Ile Thr Arg Asp Val Asp Asn Gly Gln Leu Ala Asp Asn Arg
20 25 30

Arg Thr Leu Arg Ser Gln Trp Lys Gln Val Ser Phe Phe Lys Ser Leu
35 40 45

Asp Lys Arg Leu Thr Cys Asn Asp Pro Cys Gln Met His Ser Asp Cys
50 55 60

Gly Ile Cys Glu Cys Val Glu Asn Lys Cys Ile Phe Phe Met
65 70 75

20250202

<210> 166
 <211> 27
 <212> PRT
 <213> Conus pennaceus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residues 17 and 20 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is Pro or hydroxy-Pro

<400> 166
 Leu Thr Cys Asn Asp Xaa Cys Gln Met His Ser Asp Cys Gly Ile Cys
 1 5 10 15

Xaa Cys Val Xaa Asn Lys Cys Ile Phe Phe Met
 20 25

<210> 167
 <211> 413
 <212> DNA
 <213> Conus pulicarius

<220>
 <221> CDS
 <222> (1)..(243)

<400> 167
 atg aaa ctg acg tgt gtg gtg atc gtc gcc gtg ctg ttc ctg acg gcc 48
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

tgt caa ctc agt aca gct gat gac tcc aga gat gag cag cag gat cct 96
 Cys Gln Leu Ser Thr Ala Asp Asp Ser Arg Asp Glu Gln Gln Asp Pro
 20 25 30

ttg gtg agg tcg cat cgt gag gag cag aaa gcc gag gac ccc aag acg 144
 Leu Val Arg Ser His Arg Glu Glu Gln Lys Ala Glu Asp Pro Lys Thr
 35 40 45

gcc gag aga tgt tca gat ttc gga tcc gac tgt gtt cct gct act cat 192
 Ala Glu Arg Cys Ser Asp Phe Gly Ser Asp Cys Val Pro Ala Thr His
 50 55 60

aac tgc tgc agt ggt gaa tgt ttt ggc ttc gag gac ttc ggc tta tgc 240
 Asn Cys Cys Ser Gly Glu Cys Phe Gly Phe Glu Asp Phe Gly Leu Cys
 65 70 75 80

acg taaaactggt ctgacgtctg atattccccc ctctgtcctt catcctcttt 293
 Thr

tgcttgattc atccatacct atatgtgctc ctgaaccgct gtgtaccttt accctggtgg 353

cttcagagga cggtatatca aaataaaacc gcgttgcaat gacaaaaaaaa aaaaaaaaaa 413

<210> 168
 <211> 81
 <212> PRT
 <213> Conus pulicarius

<400> 168
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

1007250202102

Cys Gln Leu Ser Thr Ala Asp Asp Ser Arg Asp Glu Gln Gln Asp Pro
 20 25 30
 Leu Val Arg Ser His Arg Glu Glu Gln Lys Ala Glu Asp Pro Lys Thr
 35 40 45
 Ala Glu Arg Cys Ser Asp Phe Gly Ser Asp Cys Val Pro Ala Thr His
 50 55 60
 Asn Cys Cys Ser Gly Glu Cys Phe Gly Phe Glu Asp Phe Gly Leu Cys
 65 70 75 80

Thr

<210> 169
 <211> 30
 <212> PRT
 <213> Conus pulicarius
 <220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residues 19 and 24 is Glu or gamma-carboxy-Glu; Xaa at residue 10 is Pro or hydroxy-Pro

<400> 169
 Cys Ser Asp Phe Gly Ser Asp Cys Val Xaa Ala Thr His Asn Cys Cys
 1 5 10 15
 Ser Gly Xaa Cys Phe Gly Phe Xaa Asp Phe Gly Leu Cys Thr
 20 25 30

<210> 170
 <211> 375
 <212> DNA
 <213> Conus purpurascens

<220>
 <221> CDS
 <222> (24)..(260)

<400> 170
 gacaggattg aacaaaattc agg atg tca aga ttt gga atc atg gtg cta acc 53
 Met Ser Arg Phe Gly Ile Met Val Leu Thr
 1 5 10
 ttt cta ctt ctt gtg tcc atg gca acc agc cat cgt tat gca aga ggg 101
 Phe Leu Leu Leu Val Ser Met Ala Thr Ser His Arg Tyr Ala Arg Gly
 15 20 25
 aag cag gcg acg cga agg aac gca atc aac atc aga cgg aga agc aca 149
 Lys Gln Ala Thr Arg Arg Asn Ala Ile Asn Ile Arg Arg Arg Ser Thr
 30 35 40
 cca aaa act gag gcg tgc gaa gag gtc tgt gag ctg gaa gaa aag cac 197
 Pro Lys Thr Glu Ala Cys Glu Glu Val Cys Glu Leu Glu Glu Lys His
 45 50 55
 tgc tgc tgc ata aga agt gac gga ccc aaa tgt tcc cgt aag tgc ctg 245
 Cys Cys Cys Ile Arg Ser Asp Gly Pro Lys Cys Ser Arg Lys Cys Leu
 60 65 70
 ttg tca atc ttc tgt tagtttctgt acactgtctc attcattatc ttatcagttac 300
 Leu Ser Ile Phe Cys

10072027001

75

aagtgtaaac gagacatgtc agaaagtcga aggttggtgcg taatttgata agtattgttt 360

gctgggatga acgga 375

<210> 171

<211> 79

<212> PRT

<213> Conus purpurascens

<400> 171

Met Ser Arg Phe Gly Ile Met Val Leu Thr Phe Leu Leu Leu Val Ser
1 5 10 15Met Ala Thr Ser His Arg Tyr Ala Arg Gly Lys Gln Ala Thr Arg Arg
20 25 30Asn Ala Ile Asn Ile Arg Arg Arg Ser Thr Pro Lys Thr Glu Ala Cys
35 40 45Glu Glu Val Cys Glu Leu Glu Glu Lys His Cys Cys Cys Ile Arg Ser
50 55 60Asp Gly Pro Lys Cys Ser Arg Lys Cys Leu Leu Ser Ile Phe Cys
65 70 75

<210> 172

<211> 37

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residues 4, 7, 8, 11, 13 and 14 is Glu or gamma-carboxy-Glu;
Xaa at residues 3 and 25 is Pro or hydroxy-Pr

<400> 172

Xaa Lys Thr Xaa Ala Cys Xaa Xaa Val Cys Xaa Leu Xaa Xaa Lys His
1 5 10 15Cys Cys Cys Ile Arg Ser Asp Gly Xaa Lys Cys Ser Arg Lys Cys Leu
20 25 30Leu Ser Ile Phe Cys
35

<210> 173

<211> 373

<212> DNA

<213> Conus purpurascens

<220>

<221> CDS

<222> (24)..(260)

<400> 173

gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53
Met Ser Gly Leu Gly Ile Met Val Leu Thr
1 5 10ctt cta ctt ctt gtg tcc atg gca acc aac cat cag gat aga gga gag 101
Leu Leu Leu Leu Val Ser Met Ala Thr Asn His Gln Asp Arg Gly Glu
15 20 25

aag cag gtg acg caa agg gac gca atc aac gtc aga cgg aga aga tca 149
 Lys Gln Val Thr Gln Arg Asp Ala Ile Asn Val Arg Arg Arg Arg Ser
 30 35 40

atc acc cag caa gtc gta tct gag gag tgc aaa aag tac tgt aag aaa 197
 Ile Thr Gln Gln Val Val Ser Glu Glu Cys Lys Lys Tyr Cys Lys Lys
 45 50 55

cag aac aag aat tgc tgc agc agt aaa cat gaa gaa ccc aga tgt gcc 245
 Gln Asn Lys Asn Cys Cys Ser Ser Lys His Glu Glu Pro Arg Cys Ala
 60 65 70

aag ata tgc ttc gga tagtttctgt acacggtctc attcattatt ttatcagtac 300
 Lys Ile Cys Phe Gly
 75

aagttaaacg agacctatca gaagtcgaag gttgtgcata atttgataaa cattgtttgc 360

tgggatgaac gga 373

<210> 174
 <211> 79
 <212> PRT
 <213> Conus purpurascens

<400> 174
 Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Ser
 1 5 10 15

Met Ala Thr Asn His Gln Asp Arg Gly Glu Lys Gln Val Thr Gln Arg
 20 25 30

Asp Ala Ile Asn Val Arg Arg Arg Arg Ser Ile Thr Gln Gln Val Val
 35 40 45

Ser Glu Glu Cys Lys Lys Tyr Cys Lys Lys Gln Asn Lys Asn Cys Cys
 50 55 60

Ser Ser Lys His Glu Glu Pro Arg Cys Ala Lys Ile Cys Phe Gly
 65 70 75

<210> 175
 <211> 32
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residues 4, 5, 23 and 24 is Glu or gamma-carboxy-Glu; Xaa
 at residue 25 is Pro or hydroxy-Pro; Xaa at residue 9 is Tyr, 125
 I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 175
 Val Val Ser Xaa Xaa Cys Lys Lys Xaa Cys Lys Lys Gln Asn Lys Asn
 1 5 10 15

Cys Cys Ser Ser Lys His Xaa Xaa Xaa Arg Cys Ala Lys Ile Cys Phe
 20 25 30

<210> 176
 <211> 24
 <212> PRT
 <213> Conus purpurascens

<220>

174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000

<221> PEPTIDE
 <222> (1)..(24)
 <223> Xaa at residue 8 is Glu or gamma-carboxy-Glu; Xaa at residue 12 is Pro or hydroxy-Pro; Xaa at residue 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 176
 Asp Cys Cys Gly Val Lys Leu Xaa Met Cys His Xaa Cys Leu Cys Asp
 1 5 10 15

Asn Ser Cys Lys Asn Xaa Gly Lys
 20

<210> 177
 <211> 235
 <212> DNA
 <213> Conus purpurascens

<220>
 <221> CDS
 <222> (1)..(204)

<400> 177
 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

ttc act tca gat cgt gca tcg gat gac agg aat acc aac gac aaa gca 96
 Phe Thr Ser Asp Arg Ala Ser Asp Asp Arg Asn Thr Asn Asp Lys Ala
 20 25 30

tct cgc ctg ctc tct cac gtt gtc agg gga tgc tgt ggt agc tat ccc 144
 Ser Arg Leu Leu Ser His Val Val Arg Gly Cys Cys Gly Ser Tyr Pro
 35 40 45

aat gct gcc tgt cat cct tgc ggt tgt aaa gat agg cca tcg tat tgt 192
 Asn Ala Ala Cys His Pro Cys Gly Cys Lys Asp Arg Pro Ser Tyr Cys
 50 55 60

ggt caa gga cgc tgatgctcca ggaccctctg aaccacgacg t 235
 Gly Gln Gly Arg
 65

<210> 178
 <211> 68
 <212> PRT
 <213> Conus purpurascens

<400> 178
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Thr Ser Asp Arg Ala Ser Asp Asp Arg Asn Thr Asn Asp Lys Ala
 20 25 30

Ser Arg Leu Leu Ser His Val Val Arg Gly Cys Cys Gly Ser Tyr Pro
 35 40 45

Asn Ala Ala Cys His Pro Cys Gly Cys Lys Asp Arg Pro Ser Tyr Cys
 50 55 60

Gly Gln Gly Arg
 65

<210> 179

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<400> 181
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15
Phe Thr Val Asp Arg Ala Thr Asp Gly Arg Ser Ala Ala Ala Ile Ala
20 25 30
Phe Ala Leu Ile Ala Pro Thr Val Arg Glu Gly Cys Cys Ser Asn Pro
35 40 45
Ala Cys His Pro Cys Gly Cys Lys Asp Arg Pro Ser Tyr Cys Gly Gln
50 55 60

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Gly Arg
65

<210> 182
<211> 23
<212> PRT
<213> Conus purpurascens

<220>
<221> PEPTIDE
<222> (1)..(23)
<223> Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residues 7, 11 and 18 is Pro or hydroxy-Pro; Xaa at residue 20 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 182
Xaa Gly Cys Cys Ser Asn Xaa Ala Cys His Xaa Cys Gly Cys Lys Asp
1 5 10 15

Arg Xaa Ser Xaa Cys Gly Gln
20

<210> 183
<211> 334
<212> DNA
<213> Conus purpurascens

<220>
<221> CDS
<222> (1)..(261)

<400> 183
atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
1 5 10 15

ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca cgc 96
Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
20 25 30

ctg acg agg gac ttc tat cgt act ctg cca gtg tct act aga gga tgc 144
Leu Thr Arg Asp Phe Tyr Arg Thr Leu Pro Val Ser Thr Arg Gly Cys
35 40 45

agc ggc tcc cct tgt ttt aaa aac aaa acg tgt cgg gat gaa tgc ata 192
Ser Gly Ser Pro Cys Phe Lys Asn Lys Thr Cys Arg Asp Glu Cys Ile
50 55 60

tgc ggc ggc tta tcc aat tgt tgg tgt ggc tac ggc ggt agt cga gga 240
Cys Gly Gly Leu Ser Asn Cys Trp Cys Gly Tyr Gly Gly Ser Arg Gly
65 70 75 80

tgc aag tgt aca tgt aga gag tgattaatcg actctttaac tcgttgaatt 291
Cys Lys Cys Thr Cys Arg Glu
85

atttaaaaaa tccagagcaa tatgttcgag aaaaaccgaa gac 334

<210> 184
<211> 87
<212> PRT
<213> Conus purpurascens

<400> 184

10073602200100

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
 20 25 30
 Leu Thr Arg Asp Phe Tyr Arg Thr Leu Pro Val Ser Thr Arg Gly Cys
 35 40 45
 Ser Gly Ser Pro Cys Phe Lys Asn Lys Thr Cys Arg Asp Glu Cys Ile
 50 55 60
 Cys Gly Gly Leu Ser Asn Cys Trp Cys Gly Tyr Gly Gly Ser Arg Gly
 65 70 75 80
 Cys Lys Cys Thr Cys Arg Glu
 85

<210> 185
 <211> 41
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(41)
 <223> Xaa at residue 16 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at residue 26 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 185
 Gly Cys Ser Gly Ser Xaa Cys Phe Lys Asn Lys Thr Cys Arg Asp Xaa
 1 5 10 15
 Cys Ile Cys Gly Gly Leu Ser Asn Cys Xaa Cys Gly Xaa Gly Gly Ser
 20 25 30
 Arg Gly Cys Lys Cys Thr Cys Arg Xaa
 35 40

<210> 186
 <211> 327
 <212> DNA
 <213> Conus purpurascens

<220>
 <221> CDS
 <222> (29)..(256)

<400> 186
 cgacctcaag agggatcgat agcagttc atg atg tct aaa ctg gga gcc ttg 52
 Met Met Ser Lys Leu Gly Ala Leu
 1 5
 ttg acc atc tgt ctg ctt ctg ttt ccc att act gct ctt ctg atg gat 100
 Leu Thr Ile Cys Leu Leu Phe Pro Ile Thr Ala Leu Leu Met Asp
 10 15 20
 gga gat caa cct gca gac cga cct gca gaa cgt atg gat tac gac att 148
 Gly Asp Gln Pro Ala Asp Arg Pro Ala Glu Arg Met Asp Tyr Asp Ile
 25 30 35 40
 tca tct gag gtg cat cgt ttg ctt gaa agg aga cac ccg ccc tgt tgc 196
 Ser Ser Glu Val His Arg Leu Leu Glu Arg Arg His Pro Pro Cys Cys

16073603-024103

45 50 55
 atg tac ggc aga tgc cgt cga tat ccc gga tgc tct agt gcc tct tgt. 244
 Met Tyr Gly Arg Cys Arg Arg Tyr Pro Gly Cys Ser Ser Ala Ser Cys
 60 65 70

tgc cag gga gga taacgtgttg atgaccaact ttgttacacg gctacgtcaa 296
 Cys Gln Gly Gly
 75

gtgtctactg aataagtaaa acgattgcag t 327

<210> 187
 <211> 76
 <212> PRT
 <213> Conus purpurascens

<400> 187
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Ile Thr Ala Leu Leu Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Asp Tyr Asp Ile Ser Ser Glu Val His Arg Leu Leu
 35 40 45
 Glu Arg Arg His Pro Pro Cys Cys Met Tyr Gly Arg Cys Arg Arg Tyr
 50 55 60
 Pro Gly Cys Ser Ser Ala Ser Cys Cys Gln Gly Gly
 65 70 75

<210> 188
 <211> 24
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(24)
 <223> Xaa at residues 2, 3 and 14 is Pro or hydroxy-Pro; Xaa at residue
 s 7 and 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho
 -Tyr or O-phospho-Tyr

<400> 188
 His Xaa Xaa Cys Cys Met Xaa Gly Arg Cys Arg Arg Xaa Xaa Gly Cys
 1 5 10 15

Ser Ser Ala Ser Cys Cys Gln Gly
 20

<210> 189
 <211> 24
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(24)
 <223> Xaa at residues 2, 3, 12 and 14 is Pro or hydroxy-Pro; Xaa at res
 idues 7 and 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
 lpho-Tyr or O-phospho-Tyr

<400> 189

Gly Xaa Xaa Cys Cys Leu Xaa Gly Ser Cys Arg Xaa Phe Xaa Gly Cys
1 5 10 15

Xaa Asn Ala Leu Cys Cys Arg Lys
20

<210> 190
<211> 400
<212> DNA
<213> Conus quercinus

<220>
<221> CDS
<222> (7)..(237)

<400> 190
ggatcc atg aaa ctg acg tgc gtg gtg atc atc gcc gtg ctg ttt ctg 48
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu
1 5 10

aca gcc agt cag ctc gtt aca gct gat tac acc aga gat aaa tgg caa 96
Thr Ala Ser Gln Leu Val Thr Ala Asp Tyr Thr Arg Asp Lys Trp Gln
15 20 25 30

tac cct gca gcg agt ttg aga ggc gga atg tgg aat ttg aga gat acc 144
Tyr Pro Ala Ala Ser Leu Arg Gly Gly Met Trp Asn Leu Arg Asp Thr
35 40 45

agg gcg tgc tcg caa gta ggt gaa gct tgt ttt cct cag aaa cct tgc 192
Arg Ala Cys Ser Gln Val Gly Glu Ala Cys Phe Pro Gln Lys Pro Cys
50 55 60

tgc cct gga ttc ctt tgc aat cac atc gga ggc atg tgc cac cac 237
Cys Pro Gly Phe Leu Cys Asn His Ile Gly Gly Met Cys His His
65 70 75

tagtaacagt ctggcatctg atatttcccc tctgcgctcc accctctttt ggctgattca 297

tccttacctg tgtgtggtca tgaaccactc agtagctaca cctctggtgg cttcagagga 357

cgtatatcaa aataaaacca cattgcaaaa aaaaaaaaaa aaa 400

<210> 191
<211> 77
<212> PRT
<213> Conus quercinus

<400> 191
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Ser Gln Leu Val Thr Ala Asp Tyr Thr Arg Asp Lys Trp Gln Tyr Pro
20 25 30

Ala Ala Ser Leu Arg Gly Gly Met Trp Asn Leu Arg Asp Thr Arg Ala
35 40 45

Cys Ser Gln Val Gly Glu Ala Cys Phe Pro Gln Lys Pro Cys Cys Pro
50 55 60

Gly Phe Leu Cys Asn His Ile Gly Gly Met Cys His His
65 70 75

<210> 192
<211> 30

10073602-001102

<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(30)
<223> Xaa at residue 7 is Glu or gamma-carboxy-Glu; Xaa at residues 11,
14 and 17 is Pro or hydroxy-Pro

<400> 192
Ala Cys Ser Gln Val Gly Xaa Ala Cys Phe Xaa Gln Lys Xaa Cys Cys
1 5 10 15

Xaa Gly Phe Leu Cys Asn His Ile Gly Gly Met Cys His His
20 25 30

<210> 193
<211> 11
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(11)
<223> Xaa at residue 4 is Pro or hydroxy-Pro

<400> 193
Asp Cys Gln Xaa Cys Gly His Asn Val Cys Cys
1 5 10

<210> 194
<211> 336
<212> DNA
<213> Conus radiatus

<220>
<221> CDS
<222> (2)..(241)

<400> 194
c atg aac tgt ctc gta ctg gct ttg gtt acc atc ggt ctt ctg gct gca 49
Met Asn Cys Leu Val Leu Ala Leu Val Thr Ile Gly Leu Leu Ala Ala
1 5 10 15

aca acc gca gcc cct ctg gac acc acc acg gtc ctc ctc agc aca act 97
Thr Thr Ala Ala Pro Leu Asp Thr Thr Thr Val Leu Leu Ser Thr Thr
20 25 30

aca cgc gat gtc aag ggc tgt gtg tac gag ggc ata gag tac agt gtc 145
Thr Arg Asp Val Lys Gly Cys Val Tyr Glu Gly Ile Glu Tyr Ser Val
35 40 45

gga gag acc tac cag gca gac tgc aac acg tgt cgc tgt gat ggc ttt 193
Gly Glu Thr Tyr Gln Ala Asp Cys Asn Thr Cys Arg Cys Asp Gly Phe
50 55 60

gac ctg gct aca tgc acc gtc gcg ggc tgc aca ggc ttt gga ccc gag 241
Asp Leu Ala Thr Cys Thr Val Ala Gly Cys Thr Gly Phe Gly Pro Glu
65 70 75 80

tgattggtac tattccacac ctacgaatgt tcacactgga accggaactt gatactacct 301

tctaaatata atcaatttgt ttcaaaaggc ccaaa 336

<210> 195

20250324

<211> 80
 <212> PRT
 <213> Conus radiatus

<400> 195
 Met Asn Cys Leu Val Leu Ala Leu Val Thr Ile Gly Leu Leu Ala Ala
 1 5 10 15
 Thr Thr Ala Ala Pro Leu Asp Thr Thr Thr Val Leu Leu Ser Thr Thr
 20 25 30
 Thr Arg Asp Val Lys Gly Cys Val Tyr Glu Gly Ile Glu Tyr Ser Val
 35 40 45
 Gly Glu Thr Tyr Gln Ala Asp Cys Asn Thr Cys Arg Cys Asp Gly Phe
 50 55 60
 Asp Leu Ala Thr Cys Thr Val Ala Gly Cys Thr Gly Phe Gly Pro Glu
 65 70 75 80

<210> 196
 <211> 43
 <212> PRT
 <213> Conus radiatus

<220>
 <221> PEPTIDE
 <222> (1)..(43)
 <223> Xaa at residues 5, 8, 13 and 43 is Glu or gamma-carboxy-Glu; Xaa
 at residue 42 is Pro or hydroxy-Pro; Xaa at residues 4,9 and 15 i
 s Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-ph
 ospo-Tyr

<400> 196
 Gly Cys Val Xaa Xaa Gly Ile Xaa Xaa Ser Val Gly Xaa Thr Xaa Gln
 1 5 10 15
 Ala Asp Cys Asn Thr Cys Arg Cys Asp Gly Phe Asp Leu Ala Thr Cys
 20 25 30
 Thr Val Ala Gly Cys Thr Gly Phe Gly Xaa Xaa
 35 40

<210> 197
 <211> 536
 <212> DNA
 <213> Conus radiatus

<220>
 <221> CDS
 <222> (87)..(296)

<400> 197
 gtgagagtcc aacagcccaa acctttcaac tcactatgtg gcagttgcag ttttcaacgt 60
 ctggacagga ttcaacaaaa ttcagg atg tca gga ttg gga atc atg gtg cta 113
 Met Ser Gly Leu Gly Ile Met Val Leu
 1 5
 acc ctt cta ctt ctt gtg tcc atg gca acc agt cgt cag gat aga gga 161
 Thr Leu Leu Leu Leu Val Ser Met Ala Thr Ser Arg Gln Asp Arg Gly
 10 15 20 25
 gtg gga cag ctg atg cca cgc gtc tcg ttc aaa gcc tgc aaa tca aat 209
 Val Gly Gln Leu Met Pro Arg Val Ser Phe Lys Ala Cys Lys Ser Asn

				30					35						40				
tat	gat	tgc	ccc	cag	cgt	ttc	aaa	tgc	tgc	agt	tac	acc	tgg	aat	gga				
Tyr	Asp	Cys	Pro	Gln	Arg	Phe	Lys	Cys	Cys	Ser	Tyr	Thr	Trp	Asn	Gly				257
			45					50					55						

tcc	agt	gga	tac	tgt	aaa	cgt	gtt	tgc	tat	ctt	tat	cgt	tagtgtaata						306
Ser	Ser	Gly	Tyr	Cys	Lys	Arg	Val	Cys	Tyr	Leu	Tyr	Arg							
		60					65					70							

cacaaagtga	ctctgttcat	tcctctccat	catctcttta	gaaacaacac	gggtgctgaga														366
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tcgtttcttt	gtgatgaaga	gtagtatcac	gggcagagtt	cactagagat	ctcaaatgaa														426
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aaacaagatt	atttagtaag	ttggggaaaa	tctggatctc	gaaaagattc	cttgaaaact														486
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ccgtatttaa	cacgcttgag	agatgataat	aaagaattct	gaaagacaaa															536
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<210> 198

<211> 70

<212> PRT

<213> Conus radiatus

<400> 198

Met	Ser	Gly	Leu	Gly	Ile	Met	Val	Leu	Thr	Leu	Leu	Leu	Leu	Val	Ser				
1				5					10					15					

Met	Ala	Thr	Ser	Arg	Gln	Asp	Arg	Gly	Val	Gly	Gln	Leu	Met	Pro	Arg				
			20					25					30						

Val	Ser	Phe	Lys	Ala	Cys	Lys	Ser	Asn	Tyr	Asp	Cys	Pro	Gln	Arg	Phe				
		35					40					45							

Lys	Cys	Cys	Ser	Tyr	Thr	Trp	Asn	Gly	Ser	Ser	Gly	Tyr	Cys	Lys	Arg				
	50					55					60								

Val	Cys	Tyr	Leu	Tyr	Arg														
65					70														

<210> 199

<211> 34

<212> PRT

<213> Conus radiatus

<220>

<221> PEPTIDE

<222> (1)..(34)

<223> Xaa at residue 9 is Pro or hydroxy-Pro; Xaa at residue 19 is Trp (D or L) or bromo-Trp (D or L); Xaa at residues 6, 17 and 33 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 199

Ala	Cys	Lys	Ser	Asn	Xaa	Asp	Cys	Xaa	Gln	Arg	Phe	Lys	Cys	Cys	Ser				
1				5					10					15					

Xaa	Thr	Xaa	Asn	Gly	Ser	Ser	Gly	Xaa	Cys	Lys	Arg	Val	Cys	Xaa	Leu				
			20					25					30						

Xaa Arg

<210> 200

<211> 356

<212> DNA

<213> Conus radiatus

<220>
 <221> CDS
 <222> (1)..(279)

<400> 200
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15
 ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca cac 96
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30
 ccg aag aga gag ttc caa cgt att ctg cta agg tct ggc aga aag tgc 144
 Pro Lys Arg Glu Phe Gln Arg Ile Leu Leu Arg Ser Gly Arg Lys Cys
 35 40 45
 aat ttc gac aaa tgt aaa ggt acc gga gtc tac aat tgt ggg gaa tcc 192
 Asn Phe Asp Lys Cys Lys Gly Thr Gly Val Tyr Asn Cys Gly Glu Ser
 50 55 60
 tgc tca tgc gaa ggt ttg cac agt tgt cgc tgc act tat aac atc ggt 240
 Cys Ser Cys Glu Gly Leu His Ser Cys Arg Cys Thr Tyr Asn Ile Gly
 65 70 75 80
 tct atg aag tct gga tgc gcg tgt att tgt aca tac tat taatgattaa 289
 Ser Met Lys Ser Gly Cys Ala Cys Ile Cys Thr Tyr Tyr
 85 90
 ttgactcgtt taactcgttg aacgatttaa aaaatccaga gcaatatggt cgagaaaaac 349
 cgaagac 356

<210> 201
 <211> 93
 <212> PRT
 <213> Conus radiatus

<400> 201
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
 20 25 30
 Pro Lys Arg Glu Phe Gln Arg Ile Leu Leu Arg Ser Gly Arg Lys Cys
 35 40 45
 Asn Phe Asp Lys Cys Lys Gly Thr Gly Val Tyr Asn Cys Gly Glu Ser
 50 55 60
 Cys Ser Cys Glu Gly Leu His Ser Cys Arg Cys Thr Tyr Asn Ile Gly
 65 70 75 80
 Ser Met Lys Ser Gly Cys Ala Cys Ile Cys Thr Tyr Tyr
 85 90

<210> 202
 <211> 47
 <212> PRT
 <213> Conus radiatus

<220>
 <221> PEPTIDE
 <222> (1)..(47)

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<223> Xaa at residues 17 and 22 is Glu or gamma-carboxy-Glu; Xaa at residues 13, 31, 46 and 47 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 202

Lys Cys Asn Phe Asp Lys Cys Lys Gly Thr Gly Val Xaa Asn Cys Gly
1 5 10 15

Xaa Ser Cys Ser Cys Xaa Gly Leu His Ser Cys Arg Cys Thr Xaa Asn
20 25 30

Ile Gly Ser Met Lys Ser Gly Cys Ala Cys Ile Cys Thr Xaa Xaa
35 40 45

<210> 203

<211> 338

<212> DNA

<213> *Conus radiatus*

<220>

<221> CDS

<222> (1)..(264)

<400> 203

atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
1 5 10 15

ctg gca tcc agg cag cag gaa gga gat gtc cag gca agg aaa aca cgc 96
Leu Ala Ser Arg Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
20 25 30

ctg acg agc gac ttc tat agt gtt ctg caa agg tat gga cta gga tgc 144
Leu Thr Ser Asp Phe Tyr Ser Val Leu Gln Arg Tyr Gly Leu Gly Cys
35 40 45

gct ggc act tgt ggt tca agc agc aat tgt gtt aga gat tat tgt gac 192
Ala Gly Thr Cys Gly Ser Ser Ser Asn Cys Val Arg Asp Tyr Cys Asp
50 55 60

tgc cca aaa ccc aat tgt tac tgc act ggc aaa ggc ttt cgt caa cca 240
Cys Pro Lys Pro Asn Cys Tyr Cys Thr Gly Lys Gly Phe Arg Gln Pro
65 70 75 80

gga tgc ggg tgt tca tgt ttg ggg tgattaattg gctcttttaa ctcgttgaac 294
Gly Cys Gly Cys Ser Cys Leu Gly
85

gatttaaaaa atccagagca atatgttcga gaaaaaccga agac 338

<210> 204

<211> 88

<212> PRT

<213> *Conus radiatus*

<400> 204

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
1 5 10 15

Leu Ala Ser Arg Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
20 25 30

Leu Thr Ser Asp Phe Tyr Ser Val Leu Gln Arg Tyr Gly Leu Gly Cys
35 40 45

Ala Gly Thr Cys Gly Ser Ser Ser Asn Cys Val Arg Asp Tyr Cys Asp

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50 55 60

Cys Pro Lys Pro Asn Cys Tyr Cys Thr Gly Lys Gly Phe Arg Gln Pro
65 70 75 80

Gly Cys Gly Cys Ser Cys Leu Gly
85

<210> 205
<211> 44
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (1)..(44)
<223> Xaa at residues 23, 25 and 37 is Pro or hydroxy-Pro; Xaa at residues 1, 19 and 28 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 205
Xaa Gly Leu Gly Cys Ala Gly Thr Cys Gly Ser Ser Ser Asn Cys Val
1 5 10 15

Arg Asp Xaa Cys Asp Cys Xaa Lys Xaa Asn Cys Xaa Cys Thr Gly Lys
20 25 30

Gly Phe Arg Gln Xaa Gly Cys Gly Cys Ser Cys Leu
35 40

<210> 206
<211> 375
<212> DNA
<213> Conus sponsalis

<220>
<221> CDS
<222> (24)..(260)

<400> 206
gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg ctg acc 53
Met Ser Gly Leu Gly Ile Met Val Leu Thr
1 5 10

ctt ttg ctt ctt gtg tcc atg gca acc agc cat aag gat gga gga gag 101
Leu Leu Leu Leu Val Ser Met Ala Thr Ser His Lys Asp Gly Gly Glu
15 20 25

aag cag gcg atg caa agg gac gca atc aac gtc aga ctg aga aga tca 149
Lys Gln Ala Met Gln Arg Asp Ala Ile Asn Val Arg Leu Arg Arg Ser
30 35 40

ctc act cgg aga gca gta act gag gcg tgc acg gag gac tgt aag act 197
Leu Thr Arg Arg Ala Val Thr Glu Ala Cys Thr Glu Asp Cys Lys Thr
45 50 55

cag gac aag aag tgc tgc ggc gaa atg aat gga caa cac aca tgt gcc 245
Gln Asp Lys Lys Cys Cys Gly Glu Met Asn Gly Gln His Thr Cys Ala
60 65 70

aag ata tgc ctc gga tagtctctgt acgctgtctc attcattatc tcatcagttac 300
Lys Ile Cys Leu Gly
75

aagtgtaaac gagacaggtc agaaagtcga aggttggttcg aaatttgata agcattgttt 360

actgggacga acgga

375

<210> 207

<211> 79

<212> PRT

<213> Conus sponsalis

<400> 207

Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Val Ser
1 5 10 15Met Ala Thr Ser His Lys Asp Gly Gly Glu Lys Gln Ala Met Gln Arg
20 25 30Asp Ala Ile Asn Val Arg Leu Arg Arg Ser Leu Thr Arg Arg Ala Val
35 40 45Thr Glu Ala Cys Thr Glu Asp Cys Lys Thr Gln Asp Lys Lys Cys Cys
50 55 60Gly Glu Met Asn Gly Gln His Thr Cys Ala Lys Ile Cys Leu Gly
65 70 75

<210> 208

<211> 32

<212> PRT

<213> Conus sponsalis

<220>

<221> PEPTIDE

<222> (1)..(32)

<223> Xaa at residues 4, 8 and 20 is Glu or gamma-carboxy-Glu

<400> 208

Ala Val Thr Xaa Ala Cys Thr Xaa Asp Cys Lys Thr Gln Asp Lys Lys
1 5 10 15Cys Cys Gly Xaa Met Asn Gly Gln His Thr Cys Ala Lys Ile Cys Leu
20 25 30

<210> 209

<211> 8

<212> PRT

<213> Conus stercusmuscarum

<220>

<221> PEPTIDE

<222> (1)..(8)

<223> Xaa at residues 3 and 6 is Pro or hydroxy-Pro; Xaa at residue 4 is D-Trp

<400> 209

Gly Cys Xaa Xaa Gln Xaa Val Cys
1 5

<210> 210

<211> 9

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(9)

<223> Xaa at residue 7 is Pro or hydroxy-Pro

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<222> (171)..(539)

<400> 214

cggtttctaa tacgactcac tatagggcaa gcagtggtaa caacgcagag tacgcggggg 60

gacggcagac cagctgggga ccagacagac gtcaaacagc atcgcagtca ggtgtggaga 120

tcccaagaca cccagaagaa ggagacagaa gagttatcgt tcgtaacaca atg gcc 176
Met Ala
1

atg aac atg tcg atg aca ctc tgc atg ttt gta atg gtc gtc gtg gca 224
Met Asn Met Ser Met Thr Leu Cys Met Phe Val Met Val Val Val Ala
5 10 15

gcc act gtc att gat tcc act cag tta caa gaa cca gat ctc agt cgc 272
Ala Thr Val Ile Asp Ser Thr Gln Leu Gln Glu Pro Asp Leu Ser Arg
20 25 30

atg cga cgc agc ggg cct gct gac tgt tgc agg atg aaa gag tgt tgc 320
Met Arg Arg Ser Gly Pro Ala Asp Cys Cys Arg Met Lys Glu Cys Cys
35 40 45 50

acc gac aga gtg aac gag tgt cta cag cgc tat tct ggc cgg gaa gat 368
Thr Asp Arg Val Asn Glu Cys Leu Gln Arg Tyr Ser Gly Arg Glu Asp
55 60 65

aaa ttc gtt tcg ttt tgt tat cag gag gcc aca gtc aca tgt gga tct 416
Lys Phe Val Ser Phe Cys Tyr Gln Glu Ala Thr Val Thr Cys Gly Ser
70 75 80

ttt aac gaa atc gtg ggc tgt tgc tat gga tat caa atg tgc atg ata 464
Phe Asn Glu Ile Val Gly Cys Cys Tyr Gly Tyr Gln Met Cys Met Ile
85 90 95

cga gtt gtg aaa ccg aac agt cta agt ggg gcc cat gag gcg tgc aaa 512
Arg Val Val Lys Pro Asn Ser Leu Ser Gly Ala His Glu Ala Cys Lys
100 105 110

acc gtt tct tgt ggt aac cct tgc gct tgaggtgtcc tcgcgccacg 559
Thr Val Ser Cys Gly Asn Pro Cys Ala
115 120

tcacctgtgt acagcgccgt caccagagcc ctgatcttta tgcccttata tgtctttttg 619

ctcttttcaact ctctgaagtc ttgaggtttg ttccattctt gtcaatcatc tcacgcgcat 679

ccaagtaaat aaaggtgacg tgacaaac 707

<210> 215

<211> 123

<212> PRT

<213> Conus striatus

<400> 215

Met Ala Met Asn Met Ser Met Thr Leu Cys Met Phe Val Met Val Val 1
1 5 10 15

Val Ala Ala Thr Val Ile Asp Ser Thr Gln Leu Gln Glu Pro Asp Leu 20
20 25 30

Ser Arg Met Arg Arg Ser Gly Pro Ala Asp Cys Cys Arg Met Lys Glu 35
35 40 45

Cys Cys Thr Asp Arg Val Asn Glu Cys Leu Gln Arg Tyr Ser Gly Arg 50
50 55 60

10072602.021102

<221> CDS

<222> (1)..(276)

<400> 218

atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttg acc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Leu Thr
 1 5 10 15

ctg gca tcc agc cag cag gag gga gat gtc cag gca agg aaa aca agc 96
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Ser
 20 25 30

ctg aag agc gac ttc tat cgt gct ctg aga ccg tat gac aga cag tgc 144
 Leu Lys Ser Asp Phe Tyr Arg Ala Leu Arg Pro Tyr Asp Arg Gln Cys
 35 40 45

act ttt gtc aac aat tgt caa cag aac ggt gcg tgt aac ggt gat tgc 192
 Thr Phe Val Asn Asn Cys Gln Gln Asn Gly Ala Cys Asn Gly Asp Cys
 50 55 60

tct tgc ggg gac cag att tgt aaa tgc ggt tat aga atc agt cct ggg 240
 Ser Cys Gly Asp Gln Ile Cys Lys Cys Gly Tyr Arg Ile Ser Pro Gly
 65 70 75 80

agg tca gga tgc gcg tgt act tgt aga aat gcc aaa tgaatcactt 286
 Arg Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys
 85 90

aactcggtga aagattttta aaaatccaga gctatatgtt cgagaaaaac cgaagac 343

<210> 219

<211> 92

<212> PRT

<213> Conus striolatus

<400> 219

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Leu Thr
 1 5 10 15

Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Ser
 20 25 30

Leu Lys Ser Asp Phe Tyr Arg Ala Leu Arg Pro Tyr Asp Arg Gln Cys
 35 40 45

Thr Phe Val Asn Asn Cys Gln Gln Asn Gly Ala Cys Asn Gly Asp Cys
 50 55 60

Ser Cys Gly Asp Gln Ile Cys Lys Cys Gly Tyr Arg Ile Ser Pro Gly
 65 70 75 80

Arg Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys
 85 90

<210> 220

<211> 46

<212> PRT

<213> Conus striolatus

<220>

<221> PEPTIDE

<222> (1)..(46)

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 33 is Pro or
 hydroxy-Pro; Xaa at residue 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, d
 i-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

125I-Tyr, mono-iodo-Tyr, d
 i-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

8 and 19 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 226

Asp Cys Arg Gly Xaa Asp Ala Xaa Cys Ser Ser Gly Ala Xaa Cys Cys
1 5 10 15

Asp Xaa Xaa Thr Cys Ser Ala Arg Thr Asn Arg Cys Phe
20 25

<210> 227

<211> 23

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 16 is Glu or gamma-carboxy-Glu; Xaa at residues 3, 11, 12, 22 and 23 is Pro or hydroxy-Pro; Xaa at residues 4, 5 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 227

Asn Cys Xaa Xaa Cys Val Val Xaa Cys Cys Xaa Xaa Ala Xaa Cys Xaa
1 5 10 15

Ala Ser Gly Cys Arg Xaa Xaa
20

<210> 228

<211> 205

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (1)..(186)

<400> 228

atg cac tgt ctc cca atc ttc gtc att ctt ctg ctg ctg act gca tct 48
Met His Cys Leu Pro Ile Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

gga cct agc gtt gat gcc caa ctg aag acc aaa gat gat gtg ccc ctg 96
Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys Asp Asp Val Pro Leu
20 25 30

tca tct ttc cga gat cat gca aag agt acc cta cga aga ctt cag gac 144
Ser Ser Phe Arg Asp His Ala Lys Ser Thr Leu Arg Arg Leu Gln Asp
35 40 45

aaa cag act tgc tgt ggc tat agg atg tgt gtt cct tgt ggt 186
Lys Gln Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly
50 55 60

taaccagcat gaaggatcc 205

<210> 229

<211> 62

<212> PRT

<213> Conus textile

<400> 229

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<210> 233
<211> 28
<212> PRT
<213> Conus textile
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<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 18 is Glu or gamma-carboxy-Glu; Xaa at residue 13 is Pro or hydroxy-Pro; Xaa at residues 5 and 27 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 3, 22 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 233
 Asp Cys Xaa Ser Xaa Leu Gly Ser Cys Ile Ala Xaa Ser Gln Cys Cys
 1 5 10 15
 Ser Xaa Val Cys Asp Xaa Xaa Cys Arg Leu Xaa Arg
 20 25

<210> 234
 <211> 279
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (7)..(126)
 <400> 234
 agctga cga atg aaa aat tcc gag aat gtc aag ctc agc aag aga aaa 48
 Arg Met Lys Asn Ser Glu Asn Val Lys Leu Ser Lys Arg Lys
 1 5 10
 tgt gtg gaa caa tgg aaa tac tgc acc cga gag tcc tta tgt tgc gcg 96
 Cys Val Glu Gln Trp Lys Tyr Cys Thr Arg Glu Ser Leu Cys Cys Ala
 15 20 25 30
 ggt ttg tgt ttg ttt agt ttc tgc att cta taacgctaata ccagagtcgt 146
 Gly Leu Cys Leu Phe Ser Phe Cys Ile Leu
 35 40
 atattccgtc taagctccac ctggcactgt ctggtatggt cctgccagtg actggtctca 206
 taccgcttag actctggtcc gtcttctctg caaccacagg agaacgtgca ttattacaat 266
 aaacgcatac tgc 279

<210> 235
 <211> 40
 <212> PRT
 <213> Conus textile

<400> 235
 Arg Met Lys Asn Ser Glu Asn Val Lys Leu Ser Lys Arg Lys Cys Val
 1 5 10 15
 Glu Gln Trp Lys Tyr Cys Thr Arg Glu Ser Leu Cys Cys Ala Gly Leu
 20 25 30
 Cys Leu Phe Ser Phe Cys Ile Leu
 35 40

<210> 236
 <211> 27
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE

1007236343

Gly Gln Leu Val Ser Ala Ser Ser His Tyr Ser Lys Asp Val Gln Ile

Cys Val Leu

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<220>
<221>  PEPTIDE
<222>  (1)..(29)
<223>  Xaa at residues 3 and 6 is Glu or gamma-carboxy-Glu; Xaa at residue 5 is Trp (D or L) or bromo-Trp (D or L)
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Cys Cys Gly Gln Leu Cys Leu Phe Gly Phe Cys Val Leu
20 25

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<220>
<221>  PEPTIDE
<222>  (1)..(27)
<223>  Xaa at residues 9 and 13 is Glu or gamma-carboxy-Glu; Xaa at resi
      dues 4, 7 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-
      sulpho-Tyr or O-phospho-Tyr
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Cys Gly Gly Xaa Ser Thr Xaa Cys Xaa Val Asp Ser Xaa Cys Cys Ser
1 5 10 15

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<210> 241
<211> 27
<212> PRT
<213> Conus textile
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<220>
<221>  PEPTIDE
<222>  (1)..(27)
<223>  Xaa at residues 8 and 13 is Glu or gamma-carboxy-Glu
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<400> 241
Gly Cys Asn Asn Ser Cys Gln Xaa His Ser Asp Cys Xaa Ser His Cys
1 5 10 15

Ile Cys Thr Ser Arg Gly Cys Gly Ala Val Asn
20 25

<210> 242
<211> 373
<212> DNA
<213> Conus tulipa

<220>
<221> CDS
<222> (22)..(258)

<400> 242
caggattgaa caaaattcag g atg tca gga ttg gga atc atg gtg cta acc 51
Met Ser Gly Leu Gly Ile Met Val Leu Thr 10
1 5

ctt cta ctt ctt gtg tcc atg gca acc agt cat cgt tat gca aga gaa 99
Leu Leu Leu Leu Val Ser Met Ala Thr Ser His Arg Tyr Ala Arg Glu 25
15 20

aag cag gcg acg cga agg gac gca gtc aac gtc aga cgg aga agc aga 147
Lys Gln Ala Thr Arg Arg Asp Ala Val Asn Val Arg Arg Arg Ser Arg 40
30 35

cca aaa aca aag gag tgc gaa agg tac tgt gag ctg gag gaa aag cac 195
Pro Lys Thr Lys Glu Cys Glu Arg Tyr Cys Glu Leu Glu Glu Lys His 55
45 50

tgc tgc tgc ata aga agt aac gga ccc aaa tgt tcc aga ata tgc ata 243
Cys Cys Cys Ile Arg Ser Asn Gly Pro Lys Cys Ser Arg Ile Cys Ile 70
60 65

ttc aaa ttt tgg tgt tagttttctg tacactgtcc attcattatc ttatcagtac 298
Phe Lys Phe Trp Cys 75

aagtgtaaac gagacatgac agaaagtcga aggttgtgac taatttgata agcattgttt 358
actgggacga acgga 373

<210> 243
<211> 79
<212> PRT
<213> Conus tulipa

<400> 243
Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Ser
1 5 10 15

Met Ala Thr Ser His Arg Tyr Ala Arg Glu Lys Gln Ala Thr Arg Arg
20 25 30

Asp Ala Val Asn Val Arg Arg Arg Ser Arg Pro Lys Thr Lys Glu Cys
35 40 45

Glu Arg Tyr Cys Glu Leu Glu Glu Lys His Cys Cys Cys Ile Arg Ser
50 55 60

Asn Gly Pro Lys Cys Ser Arg Ile Cys Ile Phe Lys Phe Trp Cys
65 70 75

<210> 244
<211> 37
<212> PRT

10072562162100

<213> Conus tulipa

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residues 5, 7, 11, 13 and 14 is Glu or gamma-carboxy-Glu;
Xaa at residues 1 and 25 is Pro or hydroxy-Pro; Xaa at residue 36
is Trp (D or L) or bromo-Trp (D or L);

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-
sulpho-Tyr or O-phospho-Tyr

<400> 244

Xaa Lys Thr Lys Xaa Cys Xaa Arg Xaa Cys Xaa Leu Xaa Xaa Lys His
1 5 10 15

Cys Cys Cys Ile Arg Ser Asn Gly Xaa Lys Cys Ser Arg Ile Cys Ile
20 25 30

Phe Lys Phe Xaa Cys
35

<210> 245

<211> 381

<212> DNA

<213> Conus tulipa

<220>

<221> CDS

<222> (22)..(267)

<400> 245

caggattgaa caaaattcag g atg tca gga ttg gga atc atg gtg cta acc 51
Met Ser Gly Leu Gly Ile Met Val Leu Thr
1 5 10

ctt ctc ctt ctt gtg cta atg aca acc agt cat cag gat gca gga gag 99
Leu Leu Leu Leu Val Leu Met Thr Thr Ser His Gln Asp Ala Gly Glu
15 20 25

aag cag gcg atg caa agg gac gca aag aac ttc agt cgg aga aga tta 147
Lys Gln Ala Met Gln Arg Asp Ala Lys Asn Phe Ser Arg Arg Arg Leu
30 35 40

gtc att cgg aga cca aaa aca agg gag tgc gaa atg cag tgt gag cag 195
Val Ile Arg Arg Pro Lys Thr Arg Glu Cys Glu Met Gln Cys Glu Gln
45 50 55

gag gag aaa cac tgc tgc cgc gta aga gat ggt acg ggc caa tgt gcc 243
Glu Glu Lys His Cys Cys Arg Val Arg Asp Gly Thr Gly Gln Cys Ala
60 65 70

cct aag tgc ttg gga att aac tgg tagtttctgt acactgtctc attcattatc 297
Pro Lys Cys Leu Gly Ile Asn Trp
75 80

ttatcagtac acgtgtaacg agacatgtca gaaagtcgaa ggtagtgcggt aatttgataa 357

gcattgttta ctgggacgaa cgga 381

<210> 246

<211> 82

10072922.0340

<212> PRT
<213> Conus tulipa

<400> 246
Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Leu
1 5 10 15
Met Thr Thr Ser His Gln Asp Ala Gly Glu Lys Gln Ala Met Gln Arg
20 25 30
Asp Ala Lys Asn Phe Ser Arg Arg Arg Leu Val Ile Arg Arg Pro Lys
35 40 45
Thr Arg Glu Cys Glu Met Gln Cys Glu Gln Glu Glu Lys His Cys Cys
50 55 60
Arg Val Arg Asp Gly Thr Gly Gln Cys Ala Pro Lys Cys Leu Gly Ile
65 70 75 80
Asn Trp

<210> 247
<211> 36
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (1)..(36)
<223> Xaa at residues 5, 7, 11, 13 and 14 is Glu or gamma-carboxy-Glu;
Xaa at residues 1 and 29 is Pro or hydroxy-Pro; Xaa at residue 36
is Trp (D or L) or bromo-Trp (D or L)

<400> 247
Xaa Lys Thr Arg Xaa Cys Xaa Met Gln Cys Xaa Gln Xaa Xaa Lys His
1 5 10 15
Cys Cys Arg Val Arg Asp Gly Thr Gly Gln Cys Ala Xaa Lys Cys Leu
20 25 30
Gly Ile Asn Xaa
35

<210> 248
<211> 363
<212> DNA
<213> Conus tulipa

<220>
<221> CDS
<222> (1)..(264)

<400> 248
atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
1 5 10 15
ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca cgc 96
Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
20 25 30
ctg aag agc gac ttc tat cgt gct ctg cca agg ttt ggc cca ata tgc 144
Leu Lys Ser Asp Phe Tyr Arg Ala Leu Pro Arg Phe Gly Pro Ile Cys
35 40 45

10072503.02102

act tgt ttt aaa agc cag aac tgt cgg ggt tct tgt gaa tgc atg tca 192
 Thr Cys Phe Lys Ser Gln Asn Cys Arg Gly Ser Cys Glu Cys Met Ser
 50 55 60

cct ccc ggt tgt tac tgc agt aac aat ggc att cgt gaa cga gga tgc 240
 Pro Pro Gly Cys Tyr Cys Ser Asn Asn Gly Ile Arg Glu Arg Gly Cys
 65 70 75 80

tcg tgt aca tgt cca ggg act ggt tgaatgattt gaaaaattca gagcaatatg 294
 Ser Cys Thr Cys Pro Gly Thr Gly
 85

ttgcagaaaa accgaagacc gagacttctc acaataaatc cataaagaca ttaaaaaaaaa 354

aaaaaaaaa 363

<210> 249

<211> 88

<212> PRT

<213> Conus tulipa

<400> 249

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15

Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
 20 25 30

Leu Lys Ser Asp Phe Tyr Arg Ala Leu Pro Arg Phe Gly Pro Ile Cys
 35 40 45

Thr Cys Phe Lys Ser Gln Asn Cys Arg Gly Ser Cys Glu Cys Met Ser
 50 55 60

Pro Pro Gly Cys Tyr Cys Ser Asn Asn Gly Ile Arg Glu Arg Gly Cys
 65 70 75 80

Ser Cys Thr Cys Pro Gly Thr Gly
 85

<210> 250

<211> 44

<212> PRT

<213> Conus tulipa

<220>

<221> PEPTIDE

<222> (1)..(44)

<223> Xaa at residues 18 and 34 is Glu or gamma-carboxy-Glu; Xaa at residues 3, 22, 23 and 42 is Pro or hydroxy-Pro; Xaa at residue 26 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 250

Phe Gly Xaa Ile Cys Thr Cys Phe Lys Ser Gln Asn Cys Arg Gly Ser
 1 5 10 15

Cys Xaa Cys Met Ser Xaa Xaa Gly Cys Xaa Cys Ser Asn Asn Gly Ile
 20 25 30

Arg Xaa Arg Gly Cys Ser Cys Thr Cys Xaa Gly Thr
 35 40

<210> 251

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<211> 383
 <212> DNA
 <213> Conus tulipa

<220>
 <221> CDS
 <222> (1)..(276)

<400> 251
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15
 ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca cgc 96
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
 20 25 30
 ctg aag agc gac ttc tat cgt act ctg gca ata tct gac aga gga tgc 144
 Leu Lys Ser Asp Phe Tyr Arg Thr Leu Ala Ile Ser Asp Arg Gly Cys
 35 40 45
 act ggc aac tgt gat tgg acg tgt agc ggt gat tgc agc tgc cag ggc 192
 Thr Gly Asn Cys Asp Trp Thr Cys Ser Gly Asp Cys Ser Cys Gln Gly
 50 55 60
 aca tct gac tcg tgt cac tgc att cca cca aaa tca ata ggc aac aga 240
 Thr Ser Asp Ser Cys His Cys Ile Pro Pro Lys Ser Ile Gly Asn Arg
 65 70 75 80
 tgc cgg tgt cag tgt aaa aga aaa atc gaa att gac tgattctttt 286
 Cys Arg Cys Gln Cys Lys Arg Lys Ile Glu Ile Asp
 85 90
 aactcgttga acgatttaaa aatcagacca atatgtaggc agaaaaccga agactctgag 346
 actctcgtaa taatcgtaag caaaaaaaaa aaaaaaa 383

<210> 252
 <211> 92
 <212> PRT
 <213> Conus tulipa

<400> 252
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr
 1 5 10 15
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg
 20 25 30
 Leu Lys Ser Asp Phe Tyr Arg Thr Leu Ala Ile Ser Asp Arg Gly Cys
 35 40 45
 Thr Gly Asn Cys Asp Trp Thr Cys Ser Gly Asp Cys Ser Cys Gln Gly
 50 55 60
 Thr Ser Asp Ser Cys His Cys Ile Pro Pro Lys Ser Ile Gly Asn Arg
 65 70 75 80
 Cys Arg Cys Gln Cys Lys Arg Lys Ile Glu Ile Asp
 85 90

<210> 253
 <211> 46
 <212> PRT
 <213> Conus tulipa

<220>
 <221> PEPTIDE
 <222> (1)..(46)
 <223> Xaa at residue 44 is Glu or gamma-carboxy-Glu; Xaa at residues 27
 and 28 is Pro or hydroxy-Pro; Xaa at residue 8 is Trp (D or L) o
 r bromo-Trp (D or L)

<400> 253
 Gly Cys Thr Gly Asn Cys Asp Xaa Thr Cys Ser Gly Asp Cys Ser Cys
 1 5 10 15
 Gln Gly Thr Ser Asp Ser Cys His Cys Ile Xaa Xaa Lys Ser Ile Gly
 20 25 30
 Asn Arg Cys Arg Cys Gln Cys Lys Arg Lys Ile Xaa Ile Asp
 35 40 45

<210> 254
 <211> 404
 <212> DNA
 <213> Conus virgo

<220>
 <221> CDS
 <222> (7)..(243)

<400> 254
 ggatcc atg aaa ctg acg tgt gtg gtg atc atc act gtg ctg ttc ctg 48
 Met Lys Leu Thr Cys Val Val Ile Ile Thr Val Leu Phe Leu
 1 5 10

acg gcc agt cag ctc att aca gct gat tac tcc aga gat cag cgg cag 96
 Thr Ala Ser Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Gln Arg Gln
 15 20 25 30

tac cgt gca gtg agg ttg gga gat gaa atg cgg aat ttc aaa ggt gcc 144
 Tyr Arg Ala Val Arg Leu Gly Asp Glu Met Arg Asn Phe Lys Gly Ala
 35 40 45

agg gac tgc ggg gga caa ggt gaa ggt tgt tat act caa cct tgc tgc 192
 Arg Asp Cys Gly Gly Gln Gly Glu Gly Cys Tyr Thr Gln Pro Cys Cys
 50 55 60

cct ggt ctg cgg tgc cgt ggc ggc ggt act gga gga ggc gta tgc cag 240
 Pro Gly Leu Arg Cys Arg Gly Gly Gly Thr Gly Gly Val Cys Gln
 65 70 75

ctg tagtaatagt ttggcatctg atatttcccc tctgtgctcc accctctttt 293
 Leu

gcctgattca tccttaccta tgtgtggtca tgaaccactc agtagctaca cctctgggtg 353

attcagagaa cgtatatcaa aataaaacca cattgcaata aaaaaaaaaa a 404

<210> 255
 <211> 79
 <212> PRT
 <213> Conus virgo

<400> 255
 Met Lys Leu Thr Cys Val Val Ile Ile Thr Val Leu Phe Leu Thr Ala
 1 5 10 15
 Ser Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Gln Arg Gln Tyr Arg

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	20		25		30	
Ala Val Arg Leu Gly Asp Glu Met Arg Asn Phe Lys Gly Ala Arg Asp	35	40	45			
Cys Gly Gly Gln Gly Glu Gly Cys Tyr Thr Gln Pro Cys Cys Pro Gly	50	55	60			
Leu Arg Cys Arg Gly Gly Gly Thr Gly Gly Gly Val Cys Gln Leu	65	70	75			
<210>	256					
<211>	32					
<212>	PRT					
<213>	Conus virgo					
<220>						
<221>	PEPTIDE					
<222>	(1)..(32)					
<223>	Xaa at residue 7 is Glu or gamma-carboxy-Glu; Xaa at residues 13 and 16 is Pro or hydroxy-Pro; Xaa at residue 10 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr					
<400>	256					
Asp Cys Gly Gly Gln Gly Xaa Gly Cys Xaa Thr Gln Xaa Cys Cys Xaa	1	5	10	15		
Gly Leu Arg Cys Arg Gly Gly Gly Thr Gly Gly Gly Val Cys Gln Leu	20	25	30			
<210>	257					
<211>	285					
<212>	DNA					
<213>	Conus radiatus					
<220>						
<221>	CDS					
<222>	(4)..(225)					
<400>	257					
atc atg cag aaa ctg aca atc ctg ctt ctt gtt gct gct ata ctg atg	1	5	10	15	48	
Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Ile Leu Met						
tcg acc cag gtc ctg att caa ggt ggt gga gaa aaa cgc caa aaa gtc			25	30	96	
Ser Thr Gln Val Leu Ile Gln Gly Gly Gly Glu Lys Arg Gln Lys Val	20					
aac att ttt tca aaa aga aag aca gat gct gag acc tgg tgg gag ggc			40	45	144	
Asn Ile Phe Ser Lys Arg Lys Thr Asp Ala Glu Thr Trp Trp Glu Gly	35					
gaa tgc tct aat tgg tta gga agt tgt tcg acg ccc tca aat tgc tgt			55	60	192	
Glu Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro Ser Asn Cys Cys	50					
ctc aag agt tgt aat ggg cac tgc aca ttg tgg tgatgaactc tgaccacaaa			70		245	
Leu Lys Ser Cys Asn Gly His Cys Thr Leu Trp	65					
gccatccaac atcaccgctc tcctcttcag agtcttcaag					285	
<210>	258					
<211>	74					
<212>	PRT					

<400> 258

Thr Gln Val Leu Ile Gln Gly Gly Gly Glu Lys Arg Gln Lys Val Asn
20 25 30

Ile Phe Ser Lys Arg Lys Thr Asp Ala Glu Thr Trp Trp Glu Gly Glu
35 40 45

Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro Ser Asn Cys Cys Leu
50 55 60

Lys Ser Cys Asn Gly His Cys Thr Leu Trp
65 70

<211> 31

<212> PRT

<213> Conus radiatus

$\langle 220 \rangle$

<221> PEPTIDE

<222> (1) . . (31)

<223> Xaa at residues 3 and is Glu or gamma-carboxy-Glu; Xaa at residue 16 is Pro or hydroxy-Pro; Xaa at residues 1, 2, 9 and 31 is Trp (D or L) or bromo-Trp (D or L)

<400> 259

Xaa Xaa Xaa Gly Xaa Cys Ser Asn Xaa Leu Gly Ser Cys Ser Thr Xaa
1 5 10 15

Ser Asn Cys Cys Leu Lys Ser Cys Asn Gly His Cys Thr Leu Xaa
20 25 30

<210> 260

<211> 296

<212> DNA

<213> Conus radiatus

<220>

<221> CDS

<222> (1) .. (237)

<400> 260

atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct gta ctg atg 48
Ile Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met
1 5 10 15

tcc acc cag gcc ctg att caa ggt ggt gga gga aaa cgc caa cag gca 96
Ser Thr Gln Ala Leu Ile Gln Gly Gly Gly Gly Lys Arg Gln Gln Ala
20 25 30

aag agc aag tat ttt tcc gaa aga aag gca cct gct aag cgt tgg ttt 144
Lys Ser Lys Tyr Phe Ser Glu Arg Lys Ala Pro Ala Lys Arg Trp Phe
35 40 45

gga cac gaa gaa tgc act tat tgg ttg ggg cct tgt gag gtg gac gac 192
Gly His Glu Glu Cys Thr Tyr Trp Leu Gly Pro Cys Glu Val Asp Asp
50 55 60

acg tgt tgt tct gcc agt tgt gag tcc aag ttc tgc ggg ttg tgg 237
Thr Cys Cys Ser Ala Ser Cys Glu Ser Lys Phe Cys Gly Leu Trp

<210>	266
<211>	381
<212>	DNA

<213> Conus regius

<220>

<221> CDS

<222> (7)..(240)

<400> 266

ggatcc atg aaa ctg acg tgc gtg gtg atc atg gcc tcg ctg ttc ctg 48
Met Lys Leu Thr Cys Val Val Ile Met Ala Ser Leu Phe Leu
1 5 10

gcg gcc tgt caa ttc ctt aca gct gga ggt gac tca aga agt aag cag 96
Ala Ala Cys Gln Phe Leu Thr Ala Gly Gly Asp Ser Arg Ser Lys Gln
15 20 25 30

cgg tat cct gat tgg agg ctg ggc tac cga aag tcc aag ttg atg gct 144
Arg Tyr Pro Asp Trp Arg Leu Gly Tyr Arg Lys Ser Lys Leu Met Ala
35 40 45

aag aag acg tgc ctg gaa cat aac aaa cta tgt tgg tat gat aga gac 192
Lys Lys Thr Cys Leu Glu His Asn Lys Leu Cys Trp Tyr Asp Arg Asp
50 55 60

tgc tgc acc ata tat tgt aat gaa aac aaa tgc ggc gtg aaa cct caa 240
Cys Cys Thr Ile Tyr Cys Asn Glu Asn Lys Cys Gly Val Lys Pro Gln
65 70 75

tgaatgtttc acacacacac acacacacac acacacacac acacacacac acacacacac 300

acacacacac atctggcgtc tgaccattcc ccctctgtgc tctatcctct tgttcctgag 360

tcattccatac ctgtgctcga g 381

<210> 267

<211> 78

<212> PRT

<213> Conus regius

<400> 267

Met Lys Leu Thr Cys Val Val Ile Met Ala Ser Leu Phe Leu Ala Ala
1 5 10 15

Cys Gln Phe Leu Thr Ala Gly Gly Asp Ser Arg Ser Lys Gln Arg Tyr
20 25 30

Pro Asp Trp Arg Leu Gly Tyr Arg Lys Ser Lys Leu Met Ala Lys Lys
35 40 45

Thr Cys Leu Glu His Asn Lys Leu Cys Trp Tyr Asp Arg Asp Cys Cys
50 55 60

Thr Ile Tyr Cys Asn Glu Asn Lys Cys Gly Val Lys Pro Gln
65 70 75

<210> 268

<211> 30

<212> PRT

<213> Conus regius

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residues 4 and 22 is Glu or gamma-carboxy-Glu; Xaa at residue 29 is Pro or hydroxy-Pro; Xaa at residue 10 is Trp (D or L) or bromo-Trp (D or L); Xaa at residues 11 and 19 is Tyr, 125I-Tyr,

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<400> 268
Thr Cys Leu Xaa His Asn Lys Leu Cys Xaa Xaa Asp Arg Asp Cys Cys
1          5          10          15
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<210>	269
<211>	285
<212>	DNA
<213>	Conus radiatus

```
<220>
<221> CDS
<222> (1)..(225)
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[illegible]

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<210> 270
<211> 75
<212> PRT
<213> Conus radiatus
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<400> 270
Ile Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Ile Leu Met
1 5 10 15
Ser Thr Gln Val Leu Ile Gln Gly Gly Gly Glu Lys Arg Gln Lys Val
20 25 30
Asn Ile Phe Ser Lys Arg Lys Thr Asp Ala Glu Thr Trp Trp Glu Gly
35 40 45
Glu Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro Ser Asn Cys Cys
50 55 60
Leu Lys Ser Cys Asn Gly His Cys Thr Leu Trp
65 70 75

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$\langle 210 \rangle$	271
$\langle 211 \rangle$	31

<212> PRT
 <213> Conus radiatus

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residues 3 and 5 is Glu or gamma-carboxy-Glu; Xaa at residue 16 is Pro or hydroxy-Pro; Xaa at residues 1,2, 9 and 31 is Trp (D or L) or bromo-Trp (D or L)

<400> 271
 Xaa Xaa Xaa Gly Xaa Cys Ser Asn Xaa Leu Gly Ser Cys Ser Thr Xaa
 1 5 10 15
 Ser Asn Cys Cys Leu Lys Ser Cys Asn Gly His Cys Thr Leu Xaa
 20 25 30

<210> 272
 <211> 296
 <212> DNA
 <213> Conus radiatus

<220>
 <221> CDS
 <222> (4)..(237)

<400> 272
 atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct gta ctg atg 48
 Met Gln Lys Leu Ile Ile Leu Leu Val Ala Ala Val Leu Met 15
 1 5 10
 tcc acc cag gcc ctg att caa ggt ggt gga gga aaa cgc caa cag gca 96
 Ser Thr Gln Ala Leu Ile Gln Gly Gly Gly Lys Arg Gln Gln Ala 30
 20 25
 aag agc aag tat ttt tcc gaa aga aag gca cct gct aag cgt tgg ttt 144
 Lys Ser Lys Tyr Phe Ser Glu Arg Lys Ala Pro Ala Lys Arg Trp Phe 45
 35 40
 gga cac gaa gaa tgc act tat tgg ttg ggg cct tgt gag gtg gac gac 192
 Gly His Glu Glu Cys Thr Tyr Trp Leu Gly Pro Cys Glu Val Asp Asp 60
 50 55
 acg tgt tgt tct gcc agt tgt gag tcc aag ttc tgc ggg ttg tgg 237
 Thr Cys Cys Ser Ala Ser Cys Glu Ser Lys Phe Cys Gly Leu Trp 75
 65 70
 tgatggacac tgaccacaag tcatactaca tcgccactct cctgttcaga gtcttcaag 296

<210> 273
 <211> 78
 <212> PRT
 <213> Conus radiatus

<400> 273
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
 1 5 10 15
 Thr Gln Ala Leu Ile Gln Gly Gly Gly Lys Arg Gln Gln Ala Lys
 20 25 30
 Ser Lys Tyr Phe Ser Glu Arg Lys Ala Pro Ala Lys Arg Trp Phe Gly
 35 40 45
 His Glu Glu Cys Thr Tyr Trp Leu Gly Pro Cys Glu Val Asp Asp Thr

50 55 60

Cys Cys Ser Ala Ser Cys Glu Ser Lys Phe Cys Gly Leu Trp
65 70 75

<210> 274
<211> 33
<212> PRT
<213> *Conus radiatus*

<220>
<221> PEPTIDE
<222> (1)..(33)
<223> Xaa at residues 5, 6, 15 and 26 is Glu or gamma-carboxy-Glu; Xaa at residue 13 is Pro or hydroxy-Pro; Xaa at residues 1, 10 and 33 is Trp (D or L) or bromo-Trp (D or L);

<220>
<221> PEPTIDE
<222> (1)..(33)
<223> Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 274
Xaa Phe Gly His Xaa Xaa Cys Thr Xaa Xaa Leu Gly Xaa Cys Xaa Val
1 5 10 15

Asp Asp Thr Cys Cys Ser Ala Ser Cys Xaa Ser Lys Phe Cys Gly Leu
20 25 30

Xaa

<210> 275
<211> 387
<212> DNA
<213> *Conus spurius*

<220>
<221> CDS
<222> (21)..(212)

<400> 275
ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu
1 5 10

ctg ctg att cca tct gca cct agc act gat gcc cga ccg aag acc aaa 101
Leu Leu Ile Pro Ser Ala Pro Ser Thr Asp Ala Arg Pro Lys Thr Lys
15 20 25

gat gat gtg cgc ctg gca tct ttc cac ggt aag gca aag cga acc cta 149
Asp Asp Val Arg Leu Ala Ser Phe His Gly Lys Ala Lys Arg Thr Leu
30 35 40

caa ata cct agg ggg aat atc cac tgt tgc aca aaa tat cag ccg tgc 197
Gln Ile Pro Arg Gly Asn Ile His Cys Cys Thr Lys Tyr Gln Pro Cys
45 50 55

tgt tct tca cca tca taaagggaaa tgactttgat gagaccctg cgaactgtcc 252
Cys Ser Ser Pro Ser
60

ctggatgtga aatttgga aa cgagactgtt cctttcgcgc gtgttcgtgg aatttcgaat 312

ggtcgttaat aacacgctgc ctcttgcaaa ctacaatctc tctgtccttt atctgtggac 372

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tggaatgtcaa cactg

387

<210> 276
<211> 64
<212> PRT
<213> Conus spurius

<400> 276
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Pro Ser
1 5 10 15
Ala Pro Ser Thr Asp Ala Arg Pro Lys Thr Lys Asp Asp Val Arg Leu
20 25 30
Ala Ser Phe His Gly Lys Ala Lys Arg Thr Leu Gln Ile Pro Arg Gly
35 40 45
Asn Ile His Cys Cys Thr Lys Tyr Gln Pro Cys Cys Ser Ser Pro Ser
50 55 60

<210> 277
<211> 17
<212> PRT
<213> Conus spurius

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residues 11 and 16 is Pro or hydroxy-Pro; Xaa at residue 9
is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
phospho-Tyr

<400> 277
Gly Asn Ile His Cys Cys Thr Lys Xaa Gln Xaa Cys Cys Ser Ser Xaa
1 5 10 15
Ser

<210> 278
<211> 206
<212> DNA
<213> Conus nobilis

<220>
<221> CDS
<222> (1)..(183)

<400> 278
atg cgc tgt ctc cca gtc ttc gtc att ctt ctg ctg ctg act gca tct 48
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15
gca cca agc gtt gat gcc cga ccg aag acc aaa gat gat gtg ctc cgg 96
Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Val Leu Arg
20 25 30
gca tct ttc cgc gat aat gca aag agt acc cta caa aga ctt tgg aac 144
Ala Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Trp Asn
35 40 45
aaa cgc atc tgc tgc ccc ata att ctt tgg tgc tgt ggt taaccagcat 193
Lys Arg Ile Cys Cys Pro Ile Ile Leu Trp Cys Cys Gly
50 55 60
gaagttccca gga 206

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<400> 279
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1          5          10          15

Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Val Leu Arg
20          25          30

Ala Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Trp Asn
35          40          45

Lys Arg Ile Cys Cys Pro Ile Ile Leu Trp Cys Cys Gly
50          55          60

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<400> 280
Ile Cys Cys Xaa Ile Ile Leu Xaa Cys Cys
1 5 10

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<220>
<221> CDS
<222> (1)..(183)
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[illegible]

<210> 282
 <211> 61
 <212> PRT
 <213> Conus betulinus

<400> 282
 Met Arg Cys Leu Pro Val Phe Ile Ile Leu Leu Val Leu Ile Ala Ser
 1 5 10 15
 Ala Pro Thr Val Asp Ala Arg Pro Lys Ile Glu Asp Asp Glu Ser Leu
 20 25 30
 Ala Ser Phe His Xaa His Xaa Pro Pro Xaa Xaa Xaa Thr Leu Leu Asn
 35 40 45
 Lys Arg Asn Cys Cys Pro Asp Ser Pro Pro Cys Cys His
 50 55 60

<210> 283
 <211> 11
 <212> PRT
 <213> Conus betulinus

<220>
 <221> PEPTIDE
 <222> (1)..(11)
 <223> Xaa at residues 4, 7 and 8 is Pro or hydroxy-Pro

<400> 283
 Asn Cys Cys Xaa Asp Ser Xaa Xaa Cys Cys His
 1 5 10

<210> 284
 <211> 569
 <212> DNA
 <213> Conus purpurascens

<400> 284
 ggaattccaa atgatgtaat tactgactac atggatcatag tgtataccca ttgaaaaatt 60
 tctatgacat ttcagttggt agatcatcca gttccacaga tggaaagaca gagagatagt 120
 agcttgcaag tggcagcgtg ttgttaacga ccattcgaca ttccatgaac acgtgtgaaa 180
 ggagcagtct gctttccaaa tctgacatcc agggacagtt tgcaggggtc tcatccaaag 240
 tcatcttcct ttatcccaaa gtacagcacc gcatctgttt tggacagcaa ccgcgtttct 300
 tccaaaatct ttgtagggtt ctttttgcac tatcgtggaa agatgccagg ggcatatcat 360
 ctttggtctt cggatgagca tcaacgcaag gtgcagatgg aatcagcagc agaagaatga 420
 cgaagactgg cagacagcgc attctgcttg tagtcagctt ccgaattcca agccgaattc 480
 tgcagatatc catcacactg gcggccgctc gagcatgcat ctagagggcc caattcgccc 540
 tatagtgagt cgtatgacaa ttcactggc 569

<210> 285
 <211> 63
 <212> PRT
 <213> Conus purpurascens

<400> 285
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Ile Pro Ser

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1 5 10 15
 Ala Pro Cys Val Asp Ala His Pro Lys Thr Lys Asp Asp Met Pro Leu
 20 25 30
 Ala Ser Phe His Asp Asn Ala Lys Gly Thr Leu Gln Arg Phe Trp Lys
 35 40 45
 Lys Arg Gly Cys Cys Pro Lys Gln Met Arg Cys Cys Thr Leu Gly
 50 55 60

<210> 286
 <211> 12
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa at residue 4 is Pro or hydroxy-Pro

<400> 286
 Gly Cys Cys Xaa Lys Gln Met Arg Cys Cys Thr Leu
 1 5 10

<210> 287
 <211> 221
 <212> DNA
 <213> Conus ammiralis

<220>
 <221> CDS
 <222> (21)..(206)

<400> 287
 ggaagctgac tacaagcaga atg cac tgt ctc cca gtc gtc gtc att ctt ctg 53
 Met His Cys Leu Pro Val Val Val Ile Leu Leu
 1 5 10

ctg ctg act gca tct ggt gga cct agc gtt gat gcc cga ctg aag acc 101
 Leu Leu Thr Ala Ser Gly Gly Pro Ser Val Asp Ala Arg Leu Lys Thr
 15 20 25

aaa gat gat gtg ccc ctg tca tct ttc cgc gat aat aca aag agt atc 149
 Lys Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Thr Lys Ser Ile
 30 35 40

cta caa aga ctt tgg aag cga ggc aac tgc tgt gaa ttt tgg gag ttt 197
 Leu Gln Arg Leu Trp Lys Arg Gly Asn Cys Cys Glu Phe Trp Glu Phe
 45 50 55

tgc tgt gat taaccagcat gaagg 221
 Cys Cys Asp
 60

<210> 288
 <211> 62
 <212> PRT
 <213> Conus ammiralis

<400> 288
 Met His Cys Leu Pro Val Val Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

Gly Gly Pro Ser Val Asp Ala Arg Leu Lys Thr Lys Asp Asp Val Pro

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20 25 30
 Leu Ser Ser Phe Arg Asp Asn Thr Lys Ser Ile Leu Gln Arg Leu Trp
 35 40 45
 Lys Arg Gly Asn Cys Cys Glu Phe Trp Glu Phe Cys Cys Asp
 50 55 60
 <210> 289
 <211> 12
 <212> PRT
 <213> Conus ammiralis
 <220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa at residues 5 and 8 is Glu or gamma-carboxy-Glu; Xaa at residue 7 is Trp (D or L) or bromo-Trp (D or L)
 <400> 289
 Gly Asn Cys Cys Xaa Phe Xaa Xaa Phe Cys Cys Asp
 1 5 10
 <210> 290
 <211> 209
 <212> DNA
 <213> Conus dalli
 <220>
 <221> CDS
 <222> (21)..(194)
 <400> 290
 ggaagctgac tacaagcaga atg cac tgt ctc cca gtc ttc gtc att ctt ctg 53
 Met His Cys Leu Pro Val Phe Val Ile Leu Leu
 1 5 10
 ctg ctg act gca tct gga cct agc gtt gat gcc caa ccg aag acc gaa 101
 Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Gln Pro Lys Thr Glu
 15 20 25
 gtt gat gtg ccc ctg tca tct ttc cgc gat aat gca aag cgt gcc cta 149
 Val Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Arg Ala Leu
 30 35 40
 caa aga ctt ccg cgt tgc tgt gaa tat tgg aag ttg tgc tgt ggt 194
 Gln Arg Leu Pro Arg Cys Cys Glu Tyr Trp Lys Leu Cys Cys Gly
 45 50 55
 taaccagcat gaagg 209
 <210> 291
 <211> 58
 <212> PRT
 <213> Conus dalli
 <400> 291
 Met His Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
 Gly Pro Ser Val Asp Ala Gln Pro Lys Thr Glu Val Asp Val Pro Leu
 20 25 30
 Ser Ser Phe Arg Asp Asn Ala Lys Arg Ala Leu Gln Arg Leu Pro Arg
 35 40 45

4872609648
 20250924

Cys Cys Glu Tyr Trp Lys Leu Cys Cys Gly
50 55

<210> 292
<211> 9
<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (1)..(9)
<223> Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residue 5 is
Trp (D or L) or bromo-Trp (D or L); Xaa at residue 4 is Tyr, 125
I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 292
Cys Cys Xaa Xaa Xaa Lys Leu Cys Cys
1 5

<210> 293
<211> 218
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (21)..(203)

<400> 293
ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu
1 5 10
ctg cta act gca tct gca cct agc gtt gat gcc cga ccg aag gcc aaa 101
Leu Leu Thr Ala Ser Ala Pro Ser Val Asp Ala Arg Pro Lys Ala Lys
15 20 25
gat gat gtg ccc ctg gca tct ttc cgt gat aat gca aag agt acc cta 149
Asp Asp Val Pro Leu Ala Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu
30 35 40
caa aga ctt cag gac aaa cgc gtt tgc tgt ggc tat aag ttt ttt tgc 197
Gln Arg Leu Gln Asp Lys Arg Val Cys Cys Gly Tyr Lys Phe Phe Cys
45 50 55
tgt cgt taaccagcat gaagg 218
Cys Arg
60

<210> 294
<211> 61
<212> PRT
<213> Conus omaria

<400> 294
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15
Ala Pro Ser Val Asp Ala Arg Pro Lys Ala Lys Asp Asp Val Pro Leu
20 25 30
Ala Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Gln Asp
35 40 45
Lys Arg Val Cys Cys Gly Tyr Lys Phe Phe Cys Cys Arg
50 55 60

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<210> 295
 <211> 11
 <212> PRT
 <213> Conus omaria

<220>
 <221> PEPTIDE
 <222> (1)..(11)
 <223> Xaa at residue 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 295
 Val Cys Cys Gly Xaa Lys Phe Phe Cys Cys Arg
 1 5 10

<210> 296
 <211> 212
 <212> DNA
 <213> Conus aulicus

<220>
 <221> CDS
 <222> (21)..(197)

<400> 296
 ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu
 1 5 10

ctg ctg act gca tct gca cct aac gtt gat gcc caa ccg aag acc aaa 101
 Leu Leu Thr Ala Ser Ala Pro Asn Val Asp Ala Gln Pro Lys Thr Lys
 15 20 25

gat gat gtg ccc ctg gca tct ttg cac gat gat gca aag agt gca cta 149
 Asp Asp Val Pro Leu Ala Ser Leu His Asp Asp Ala Lys Ser Ala Leu
 30 35 40

caa cat tgg aac caa cgc tgc tgc ccc atg atc tat tgg tgc tgt agt 197
 Gln His Trp Asn Gln Arg Cys Cys Pro Met Ile Tyr Trp Cys Cys Ser
 45 50 55

taaccagcat gaagg 212

<210> 297
 <211> 59
 <212> PRT
 <213> Conus aulicus

<400> 297
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

Ala Pro Asn Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30

Ala Ser Leu His Asp Asp Ala Lys Ser Ala Leu Gln His Trp Asn Gln
 35 40 45

Arg Cys Cys Pro Met Ile Tyr Trp Cys Cys Ser
 50 55

<210> 298
 <211> 10
 <212> PRT

20250202

<213> Conus aulicus

<220>

<221> PEPTIDE

<222> (1)..(10)

<223> Xaa at residue 3 is Pro or hydroxy-Pro; Xaa at residue 7 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 298

Cys Cys Xaa Met Ile Xaa Xaa Cys Cys Ser
1 5 10

<210> 299

<211> 212

<212> DNA

<213> Conus aulicus

<220>

<221> CDS

<222> (21)..(197)

<400> 299

ggaagctgac tacaagcaga atg cac tgt ctc cca gtc ttc gtc att ctt ctg 53
Met His Cys Leu Pro Val Phe Val Ile Leu Leu
1 5 10

ctg ctg act gca tct gca cct aac gtt gat gcc caa ccg aag acc aaa 101
Leu Leu Thr Ala Ser Ala Pro Asn Val Asp Ala Gln Pro Lys Thr Lys
15 20 25

gat gat gtg ccc ctg gca tct ttg cac gat gat gca aag agt gca cta 149
Asp Asp Val Pro Leu Ala Ser Leu His Asp Asp Ala Lys Ser Ala Leu
30 35 40

caa cat tgg aac caa cgc tgc tgc ccc gag atc tat tgg tgc tgt agt 197
Gln His Trp Asn Gln Arg Cys Cys Pro Glu Ile Tyr Trp Cys Cys Ser
45 50 55

taaccagcat gaagg 212

<210> 300

<211> 59

<212> PRT

<213> Conus aulicus

<400> 300

Met His Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

Ala Pro Asn Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro Leu
20 25 30

Ala Ser Leu His Asp Asp Ala Lys Ser Ala Leu Gln His Trp Asn Gln
35 40 45

Arg Cys Cys Pro Glu Ile Tyr Trp Cys Cys Ser
50 55

<210> 301

<211> 10

<212> PRT

<213> Conus aulicus

<220>

2

5

3

[illegible]

nd 11 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 307

Xaa Asn Asn Xaa Cys Cys Thr Asn Xaa Leu Xaa Cys Cys
1 5 10

<210> 308

<211> 218

<212> DNA

<213> Conus dalli

<220>

<221> CDS

<222> (21)..(203)

<400> 308

ggaagctgac tacaagcaga atg cac tgt ctc cca gtc ttc gtc att ctt ctg 53
Met His Cys Leu Pro Val Phe Val Ile Leu Leu
1 5 10

ctg ctg act gca tct gga cct agc gtt gat gcc cga ccg aag acc gaa 101
Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Arg Pro Lys Thr Glu
15 20 25

gat gat gtg ccc ctg tca tct ttc cgc gat aat aca aag agt acc cta 149
Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Thr Lys Ser Thr Leu
30 35 40

caa aga ctt ttg aag cca gtc aac tgc tgt cct att gat caa tct tgc 197
Gln Arg Leu Leu Lys Pro Val Asn Cys Cys Pro Ile Asp Gln Ser Cys
45 50 55

tgt tct taaccagcat gaagg 218
Cys Ser
60

<210> 309

<211> 61

<212> PRT

<213> Conus dalli

<400> 309

Met His Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

Gly Pro Ser Val Asp Ala Arg Pro Lys Thr Glu Asp Asp Val Pro Leu
20 25 30

Ser Ser Phe Arg Asp Asn Thr Lys Ser Thr Leu Gln Arg Leu Leu Lys
35 40 45

Pro Val Asn Cys Cys Pro Ile Asp Gln Ser Cys Cys Ser
50 55 60

<210> 310

<211> 13

<212> PRT

<213> Conus dalli

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residues 1 and 6 is Pro or hydroxy-Pro

117-118-119-120-121-122-123-124-125-126-127-128-129-130-131-132-133-134-135-136-137-138-139-140-141-142-143-144-145-146-147-148-149-150-151-152-153-154-155-156-157-158-159-160-161-162-163-164-165-166-167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000

<400> 310
 Xaa Val Asn Cys Cys Xaa Ile Asp Gln Ser Cys Cys Ser
 1 5 10

<210> 311
 <211> 239
 <212> DNA
 <213> Conus consors

<220>
 <221> CDS
 <222> (7)..(228)

<400> 311
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10
 gtt tcc atc cct tca gat cgt gca tct gaa ggc agg aat gcc gta gtc 96
 Val Ser Ile Pro Ser Asp Arg Ala Ser Glu Gly Arg Asn Ala Val Val
 15 20 25 30
 cac gag aga gcg cct gag ctg gtc gtt acg gcc acc acg act tgc tgt 144
 His Glu Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys
 35 40 45
 ggt tat gat ccg atg aca ata tgc cct cct tgc atg tgc act cat tcc 192
 Gly Tyr Asp Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser
 50 55 60
 tgt cca cca aaa aga aaa cca ggc cgc aga aac gac tgatgctcga g 239
 Cys Pro Pro Lys Arg Lys Pro Gly Arg Arg Asn Asp
 65 70

<210> 312
 <211> 74
 <212> PRT
 <213> Conus consors

<400> 312
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15
 Ile Pro Ser Asp Arg Ala Ser Glu Gly Arg Asn Ala Val Val His Glu
 20 25 30
 Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr
 35 40 45
 Asp Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser Cys Pro
 50 55 60
 Pro Lys Arg Lys Pro Gly Arg Arg Asn Asp
 65 70

<210> 313
 <211> 36
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residues 2,

100266290

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<400> 315
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15
Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Val Asn Glu
20 25 30
Arg Gln Ser Trp Leu Val Pro Ser Thr Ile Thr Thr Cys Cys Gly Tyr
35 40 45
Asp Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asn Asn Thr Cys Lys
50 55 60
Pro Lys Lys Pro Lys Pro Gly Lys Gly Arg Arg Asn Asp

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75

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<400> 318
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1          5          10          15
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Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Val Val His Glu
20 25 30

Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr
35 40 45

Asp Pro Met Thr Trp Cys Pro Ser Cys Met Cys Thr Tyr Ser Cys Pro
50 55 60

His Gln Arg Lys Lys Pro Gly Arg Arg Asn Asp
65 70 75

<210> 319
<211> 37
<212> PRT
<213> Conus consors

<220>
<221> PEPTIDE
<222> (1)..(37)
<223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residues 2, 17, 22, 31 and 37 is Pro or hydroxy-Pro; Xaa at residue 20 is Trp (D or L) or bromo-Trp (D or L);

<220>
<221> PEPTIDE
<222> (1)..(37)
<223> Xaa at residues 15 and 28 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 319
Ala Xaa Xaa Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Xaa Asp
1 5 10 15

Xaa Met Thr Xaa Cys Xaa Ser Cys Met Cys Thr Xaa Ser Cys Xaa His
20 25 30

Gln Arg Lys Lys Xaa
35

<210> 320
<211> 260
<212> DNA
<213> Conus magus

<220>
<221> CDS
<222> (7)..(231)

<220>
<221> misc_feature
<222> (1)..(260)
<223> n is unknown

<400> 320
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc agt gtc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ser Val
1 5 10

gtt tcc atc cct tca gat cgt gca tct gat ggc ggg aat gcc gta gtc 96
Val Ser Ile Pro Ser Asp Arg Ala Ser Asp Gly Gly Asn Ala Val Val
15 20 25 30

cac gag aga gcg cct gag ctg gtc gtt acg gcc acc acg act tgc tgt 144

1007250202

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<210> 321
<211> 74
<212> PRT
<213> Conus magus
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<210>	322
<211>	36
<212>	PRT
<213>	Conus magus

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<400> 322
Ala Xaa Xaa Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Xaa Asp
1      5      10      15
Xaa Met Thr Ile Cys Xaa Xaa Cys Met Cys Thr His Ser Cys Xaa Xaa
      20      25      30
Lys Gly Lys Xaa
      35

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<220>
<221> CDS

<400> 323

aat gcc gca gtc aac gag aga cag aaa tgg ctg gtc cat tcg aaa atc 100
Asn Ala Ala Val Asn Glu Arg Gln Lys Trp Leu Val His Ser Lys Ile
15 20 25

acg tat tgc tgt ggt tat aat aag atg gac atg tgc cct cct tgc atg 148
Thr Tyr Cys Cys Gly Tyr Asn Lys Met Asp Met Cys Pro Pro Cys Met
30 35 40

tgc act tat tcc tgt ccc ccc cta aaa aaa aaa aga cca ggc cgc aga 196
Cys Thr Tyr Ser Cys Pro Pro Leu Lys Lys Lys Arg Pro Gly Arg Arg
45 50 55

aac gac tgatgctcca ggaccctctg aaccacgacc tcgagcgaag ggcgaattc 251
Asn Asp
60

$\langle 210 \rangle$ 324

<211> 60

<212> PRT

<213> Conus aurisiacus

<400> 324

Val Val Leu Gly Pro Glu Pro Asp Gly Arg Asn Ala Ala Val Asn Glu
1 5 10 15

Arg Gln Lys Trp Leu Val His Ser Lys Ile Thr Tyr Cys Cys Gly Tyr
20 25 30

Asn Lys Met Asp Met Cys Pro Pro Cys Met Cys Thr Tyr Ser Cys Pro
35 40 45

Pro Leu Lys Lys Lys Arg Pro Gly Arg Arg Asn Asp
50 55 60

<210> 325

<211> 38

<212> PRT

<213> Conus aurisiacus

$\langle 220 \rangle$

<221> PEPTIDE

<222> (1) .. (38)

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 22, 23, 31, 32 and 38 is Pro or hydroxy-Pro; Xaa at residue 3 is Trp (D or L) or bromo-Trp (D or L); Xaa at residues 11, 15 and 28 is Tyr, 12 5I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 325

Xaa Lys Xaa Leu Val His Ser Lys Ile Thr Xaa Cys Cys Gly Xaa Asn
1 5 10 15

Lys Met Asp Met Cys Xaa Xaa Cys Met Cys Thr Xaa Ser Cys Xaa Xaa
20 25 30

Leu Lys Lys Lys Arg Xaa
35

<210> 326

<211> 212
 <212> DNA
 <213> Conus aurisiacus

<220>
 <221> CDS
 <222> (23)..(163)

<400> 326
 gaattcgccc ttgaggatcc gt gtg gtt ctg ggt cca gca ttt gat ggc agg 52
 Val Val Leu Gly Pro Ala Phe Asp Gly Arg
 1 5 10

aat gcc gca gtc aac gag aga gcg cct tgg acg gtc gtt acg gcc acc 100
 Asn Ala Ala Val Asn Glu Arg Ala Pro Trp Thr Val Val Thr Ala Thr
 15 20 25

acg aat tgc tgc ggt att acc ggg cca ggc tgc ctt cct tgc cgt tgt 148
 Thr Asn Cys Cys Gly Ile Thr Gly Pro Gly Cys Leu Pro Cys Arg Cys
 30 35 40

act caa aca tgt ggc tgatgctcca ggaccctctg aaccacgacc tcgagcgaag 203
 Thr Gln Thr Cys Gly
 45

ggcgaattc 212

<210> 327
 <211> 47
 <212> PRT
 <213> Conus aurisiacus

<400> 327
 Val Val Leu Gly Pro Ala Phe Asp Gly Arg Asn Ala Ala Val Asn Glu
 1 5 10 15

Arg Ala Pro Trp Thr Val Val Thr Ala Thr Thr Asn Cys Cys Gly Ile
 20 25 30

Thr Gly Pro Gly Cys Leu Pro Cys Arg Cys Thr Gln Thr Cys Gly
 35 40 45

<210> 328
 <211> 29
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(29)
 <223> Xaa at residues 2, 18 and 22 is Pro or hydroxy-Pro; Xaa at residue 3 is Trp (D or L) or bromo-Trp (D or L)

<400> 328
 Ala Xaa Xaa Thr Val Val Thr Ala Thr Thr Asn Cys Cys Gly Ile Thr
 1 5 10 15

Gly Xaa Gly Cys Leu Xaa Cys Arg Cys Thr Gln Thr Cys
 20 25

<210> 329
 <211> 218
 <212> DNA
 <213> Conus marmoreus

15072503.04403

$\langle 220 \rangle$

[illegible]

ctt	ctg	ctg	ctg	act	gca	tct	gca	cct	agc	gtt	gat	gcc	aaa	gtt	cat	102
Leu	Leu	Leu	Leu	Thr	Ala	Ser	Ala	Pro	Ser	Val	Asp	Ala	Lys	Val	His	
10					15					20					25	

aag agt acc cta caa aga ctt cag gac aaa agc act tgc tgt ggc ttt 198
Lys Ser Thr Leu Gln Arg Leu Gln Asp Lys Ser Thr Cys Cys Gly Phe
45 50 55

aag atg tgt atc cct tgt agt taaccagcat gaaggatcc 238
Lys Met Cys Ile Pro Cys Ser
60

<210>	333
<211>	64
<212>	PRT
<213>	Conus pennaceus

```
<400> 333
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1          5          10          15
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Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly
20 25 30

Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu
35 40 45

Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Ser
50 55 60

<210>	334
<211>	13
<212>	PRT
<213>	Conus pennaceus

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<220>
<221>  PEPTIDE
<222>  (1)..(13)
<223>  Xaa at residue 11 is Pro or hydroxy-Pro
```

<400> 334
Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Xaa Cys Ser
1 5 10

<210>	335
<211>	231
<212>	DNA
<213>	Conus pennaceus

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<220>
<221> CDS
<222> (27)..(212)
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<210>	341
<211>	250
<212>	DNA
<213>	Conus episcopatus


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<220>
<221> CDS
<222> (82) .. (264)
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[illegible]

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<400>   345
Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
 1                               10                      15

Ala Pro Gly Val Val Val Leu Pro Lys Thr Glu Asp Asp Val Pro Met
 20                      25                      30

Ser Ser Val Tyr Gly Asn Gly Lys Ser Ile Leu Arg Gly Ile Leu Arg
 35                      40                      45

Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys His Pro Cys

```

50 55 60

<210> 346
 <211> 13
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 12 is Pro or hydroxy-Pro; Xaa at residue 7 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-
 Tyr

<400> 346
 Asn Gly Val Cys Cys Gly Xaa Lys Leu Cys His Xaa Cys
 1 5 10

<210> 347
 <211> 12
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa at residue 11 is Pro or hydroxy-Pro; Xaa at residue 6 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-
 Tyr

<400> 347
 Gly Val Cys Cys Gly Xaa Lys Leu Cys His Xaa Cys
 1 5 10

<210> 348
 <211> 202
 <212> DNA
 <213> Conus bandanus

<220>
 <221> CDS
 <222> (1)..(183)

<400> 348
 atg cgc tgt ctc cca gtc ttg atc att ctt ctg ctg ctg act gca tct 48
 Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

gca cct ggc gtt gat gtc cta ccg aag acc gaa gat gat gtg ccc ctg 96
 Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu
 20 25 30

tca tct gtc tac gat aat aca aag agt atc cta cga gga ctt ctg gac 144
 Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp
 35 40 45

aaa cgt gct tgc tgt ggc tac aag ctt tgc tca cca tgt taaccagcat 193
 Lys Arg Ala Cys Cys Gly Lys Leu Cys Ser Pro Cys
 50 55 60

gaaggatcc 202

<210> 349
 <211> 61
 <212> PRT
 <213> Conus bandanus

<400> 349

Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu
 20 25 30

Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp
 35 40 45

Lys Arg Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys
 50 55 60

<210> 350

<211> 11

<212> PRT

<213> Conus bandanus

<220>

<221> PEPTIDE

<222> (1)..(11)

<223> Xaa at residue 10 is Pro or hydroxy-Pro; Xaa at residue 5 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-
 Tyr

<400> 350

Ala Cys Cys Gly Xaa Lys Leu Cys Ser Xaa Cys
 1 5 10

<210> 351

<211> 221

<212> DNA

<213> Conus aulicus

<220>

<221> CDS

<222> (21)..(206)

<400> 351

ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu
 1 5 10

ctg ctg act gca tct gga cct agc gtt gat gcc cga ctg aag acc aaa 101
 Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Arg Leu Lys Thr Lys
 15 20 25

gat gat gtg ccc ctg tca tct ttc cga gat aat gca aag agt acc cta 149
 Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu
 30 35 40

caa aga cat cag gac aaa agc gtt tgc tgt ggc tat aag ctg tgt ttt 197
 Gln Arg His Gln Asp Lys Ser Val Cys Cys Gly Tyr Lys Leu Cys Phe
 45 50 55

cct tgt ggt taaccagcat gaagg 221
 Pro Cys Gly
 60

<210> 352

<211> 62

<212> PRT

<213> Conus aulicus

<400> 352

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 22123-20201

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
1 5 10 15

Gly Pro Ser Val Asp Ala Arg Leu Lys Thr Lys Asp Asp Val Pro Leu
20 25 30

Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg His Gln Asp
35 40 45

Lys Ser Val Cys Cys Gly Tyr Lys Leu Cys Phe Pro Cys Gly
50 55 60

<210> 353

<211> 12

<212> PRT

<213> Conus aulicus

<220>

<221> PEPTIDE

<222> (1)..(12)

<223> Xaa at residue 11 is Pro or hydroxy-Pro; Xaa at residue 6 is Tyr,
125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-
Tyr

<400> 353

Ser Val Cys Cys Gly Xaa Lys Leu Cys Phe Xaa Cys
1 5 10

<210> 354

<211> 312

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (3)..(50)

<220>

<221> misc_feature

<222> (1)..(312)

<223> n is unknown

<400> 354

ca gga tcc aat ggg gtt tgt tgt ggc tat agg atg tgt gtt cct tgt 47
Gly Ser Asn Gly Val Cys Cys Gly Tyr Arg Met Cys Val Pro Cys
1 5 10 15

ggg taaccagcat gaagggaaat gactttggat gagaccctg cgaactgtcc 100
Gly

ctggatgtga gatttggaaa gcagactgtt cattttgcac gtgttcgtgg aatttcgaat 160

ggtcgttaac aacacgctgc cacttgcaag ctactatctc tctgtccttt tatctgtgga 220

actgtatgat ctaacaactg aaatatcata nanatttttc aatgggtatn cactatgcat 280

atgatcatgt aggggttcaag ggggtcaagat nc 312

<210> 355

<211> 16

<212> PRT

<213> Conus textile

1007250234102

<210> 362
 <211> 12
 <212> PRT
 <213> *Conus ammiralis*

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 11 is Pro or hydroxy-Pro

<400> 362
 Xaa Ala Cys Cys Gly Phe Lys Met Cys Val Xaa Cys
 1 5 10

<210> 363
 <211> 211
 <212> DNA
 <213> *Conus pennaceus*

<220>
 <221> CDS
 <222> (1)..(192)

<400> 363
 atg cgc tgt ctc cca gtc ttc gtc att ctt ctg ctg ctg act gca tct 48
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

gca cct agc gtt gat gcc aaa gtt cat ctg aag acc aaa ggt gat ggg 96
 Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly
 20 25 30

ccc ctg tca tct ttc cga gat aat gca aag agt acc cta caa aga ctt 144
 Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu
 35 40 45

cag gac aaa agc act tgc tgt ggc ttt aag atg tgt att cct tgt cgt 192
 Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg
 50 55 60

taaccagcat gaaggatcc 211

<210> 364
 <211> 64
 <212> PRT
 <213> *Conus pennaceus*

<400> 364
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly
 20 25 30

Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu
 35 40 45

Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg
 50 55 60

<210> 365
 <211> 13
 <212> PRT
 <213> *Conus pennaceus*

<220>
 <221> PEPTIDE
 <222> (1)..(13) *
 <223> Xaa at residue 13 is Pro or hydroxy-Pro
 <400> 365
 Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Xaa Cys Arg
 1 5 10

<210> 366
 <211> 304
 <212> DNA
 <213> Conus pennaceus

<220>
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 <222> (3)..(50)

<220>
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 <223> n is unknown

<400> 366
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 Gly Ser Asn Gly Val Cys Cys Gly Phe Trp Met Cys Ile Pro Cys
 1 5 10 15

aat taaccagcat gaagggaaat gactttggat aagacccctg cgaactgtcc 100
 Asn

ttggatgtga gatttggaaa gcagactgtt ccttttgcac gtgttcgtgg aatttcgaat 160

ggtcgttaac aacacgctgc cacttgcaag ctactatctc tctgtccttt catctgtgga 220

actgtatgat ctaacaactg aaatatcata gaaatttttc aatgggtata cactatgcat 280

atgaccatgt angggtcaac agnc 304

<210> 367
 <211> 16
 <212> PRT
 <213> Conus pennaceus

<400> 367
 Gly Ser Asn Gly Val Cys Cys Gly Phe Trp Met Cys Ile Pro Cys Asn
 1 5 10 15

<210> 368
 <211> 14
 <212> PRT
 <213> Conus pennaceus

<220>
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 <222> (1)..(14)
 <223> Xaa at residue 12 is Pro or hydroxy-Pro; Xaa at residue 8 is Trp
 (D or L) or bromo-Trp (D or L)

<400> 368
 Asn Gly Val Cys Cys Gly Phe Xaa Met Cys Ile Xaa Cys Asn
 1 5 10

137

<210> 369
 <211> 218
 <212> DNA
 <213> Conus omaria

<220>
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 <222> (21)..(203)

<400> 369
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 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu
 1 5 10

ctg ctg act gca tct gca cct agc gtt gat gcc cga ccg aag gcc aaa 101
 Leu Leu Thr Ala Ser Ala Pro Ser Val Asp Ala Arg Pro Lys Ala Lys
 15 20 25

gat gat gtg ccc ctg tca tct ttc cgt gat aat gca aag agt acc cta 149
 Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu
 30 35 40

caa aga ctt cag gac aaa gac gtt tgc tgt tac gtt aga atg tgt cct 197
 Gln Arg Leu Gln Asp Lys Asp Val Cys Cys Tyr Val Arg Met Cys Pro
 45 50 55

tgt cgt taaccagcat gaagg 218
 Cys Arg
 60

<210> 370
 <211> 61
 <212> PRT
 <213> Conus omaria

<400> 370
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15

Ala Pro Ser Val Asp Ala Arg Pro Lys Ala Lys Asp Asp Val Pro Leu
 20 25 30

Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Gln Asp
 35 40 45

Lys Asp Val Cys Cys Tyr Val Arg Met Cys Pro Cys Arg
 50 55 60

<210> 371
 <211> 12
 <212> PRT
 <213> Conus omaria

<220>
 <221> PEPTIDE
 <222> (1)..(12)
 <223> Xaa at residue 10 is Pro or hydroxy-Pro; Xaa at residue 5 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-
 Tyr

<400> 371
 Asp Val Cys Cys Xaa Val Arg Met Cys Xaa Cys Arg
 1 5 10

<210> 372

<211> 84
 <212> PRT
 <213> *Conus radiatus*

<220>
 <221> PEPTIDE
 <222> (1)..(84)
 <223> Xaa at residues 27, 32, 38, 39 and 41 is Glu or gamma-carboxy-Glu
 ; Xaa at residues 2, 5, 17, 23, 43, 45 and 58 is Pro or hydroxy-P
 ro; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 372
 His Xaa Thr Lys Xaa Cys Met Xaa Cys Ser Phe Gly Gln Cys Val Gly
 1 5 10 15
 Xaa His Ile Cys Cys Gly Xaa Thr Gly Cys Xaa Met Gly Thr Ala Xaa
 20 25 30
 Ala Asn Met Cys Ser Xaa Xaa Asp Xaa Asp Xaa Ile Xaa Cys Gln Val
 35 40 45
 Phe Gly Ser Asp Cys Ala Leu Asn Asn Xaa Asp Asn Ile His Gly His
 50 55 60
 Cys Val Ala Asp Gly Ile Cys Cys Val Asp Asp Thr Cys Thr Thr His
 65 70 75 80
 Leu Gly Cys Leu

<210> 373
 <211> 218
 <212> DNA
 <213> *Conus tessulatus*

<220>
 <221> CDS
 <222> (7)..(174)

<400> 373
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 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10
 gtt tcc ttc agt gca gat cgt gcc aac gtc aaa gcg tct gac ctg atc 96
 Val Ser Phe Ser Ala Asp Arg Ala Asn Val Lys Ala Ser Asp Leu Ile
 15 20 25 30
 gcc cag gcc acc aga gac ggc tgt cca cca cat ccc gtt cct ggc atg 144
 Ala Gln Ala Thr Arg Asp Gly Cys Pro Pro His Pro Val Pro Gly Met
 35 40 45
 cat aag tgc atg tgt act aat aca tgt ggt tgaagacgct gatgctccag 194
 His Lys Cys Met Cys Thr Asn Thr Cys Gly
 50 55
 gaccctctga accacgacct cgag 218

<210> 374
 <211> 56
 <212> PRT
 <213> *Conus tessulatus*

<400> 374
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

234034

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<210>      375
<211>      20
<212>      PRT
<213>      Conus tessulatus

<220>
<221>      PEPTIDE
<222>      (1)..(20)
<223>      Xaa at residues 4, 5, 7 and 9 is Pro or hydroxy-Pro

<400>      375
Asp Gly Cys Xaa Xaa His Xaa Val Xaa Gly Met His Lys Cys Met Cys
1              5              10              15

Thr Asn Thr Cys
              20

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<220>
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<222> (400)..(510)

<220>
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<223> n is unknown
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nataatnggt	nggannaaga	agantaaaag	tanngnttng	tgaaanaang	annnnatggt										180	
nnanntcata	acnnnaatgt	aaataatana	cgnnccagt	tgaaannntn	tcnnnnataa										240	
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				Ser	Asp	Xaa	Arg	Asp								
				1					5							
gac aca gcc	aaa gac	gaa ggg	tct nac	atg gac	aaa ttg	gtc gag	aaa									462
Asp Thr	Ala Lys	Asp Glu	Gly Ser	Xaa Met	Asp Lys	Leu Val	Glu Lys									
				10					15					20		
aaa gaa tgt	tgc cat	cct gcc	tgt ggc	aaa cac	tac agt	tgt tga	cgc									510
Lys Glu	Cys Cys	His Pro	Ala Cys	Gly Lys	His Tyr	Ser Cys	Gly Arg									
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tgatgctcca gggtnntgaag gancaa

536

<210> 377

<211> 37

<212> PRT

<213> Conus geographus

<400> 377

Ser Asp Xaa Arg Asp Asp Thr Ala Lys Asp Glu Gly Ser Xaa Met Asp
1 5 10 15

Lys Leu Val Glu Lys Lys Glu Cys Cys His Pro Ala Cys Gly Lys His
20 25 30

Tyr Ser Cys Gly Arg
35

<210> 378

<211> 13

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residue 5 is
Pro or hydroxy-Pro; Xaa at residue 11 is Tyr, 125I-Tyr, mono-iod
o-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 378

Xaa Cys Cys His Xaa Ala Cys Gly Lys His Xaa Ser Cys
1 5 10

<210> 379

<211> 217

<212> DNA

<213> Conus geographus

<220>

<221> CDS

<222> (7)..(183)

<400> 379

ggatcc atg ttc acc gtg ttt ctg ttg gtg gtc ttg gca acc act gtc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
1 5 10

gtt tcc ttc cct tca gaa cgt gca tct gat ggc agg gat gac aca gcc 96
Val Ser Phe Pro Ser Glu Arg Ala Ser Asp Gly Arg Asp Asp Thr Ala
15 20 25 30

aaa gac gaa ggg tct gac atg gag aaa ttg gtc gag aaa aaa gaa tgt 144
Lys Asp Glu Gly Ser Asp Met Glu Lys Leu Val Glu Lys Lys Glu Cys
35 40 45

tgc aat cct gcc tgt ggc aga cac ttc agt tgt gga cgc tgatgctcca 193
Cys Asn Pro Ala Cys Gly Arg His Phe Ser Cys Gly Arg
50 55

ggaccctctg aaccacgact cgag

217

<210> 380

<211> 59

<212> PRT

4003602007

<400> 383
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15
 Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala Lys Asp
 20 25 30
 Glu Arg Ser Asp Met His Glu Ser Asp Arg Lys Gly Arg Ala Tyr Cys
 35 40 45
 Cys His Pro Ala Cys Gly Pro Asn Tyr Ser Cys Gly Thr Ser Cys Ser
 50 55 60
 Arg Thr Leu
 65

<210> 384
 <211> 22
 <212> PRT
 <213> Conus striatus
 <220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residues 6 and 10 is Pro or hydroxy-Pro; Xaa at residues 2
 and 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Ty
 r or O-phospho-Tyr

<400> 384
 Ala Xaa Cys Cys His Xaa Ala Cys Gly Xaa Asn Xaa Ser Cys Gly Thr
 1 5 10 15
 Ser Cys Ser Arg Thr Leu
 20

<210> 385
 <211> 224
 <212> DNA
 <213> Conus striatus

<220>
 <221> CDS
 <222> (7)..(189)

<400> 385
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 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10
 gtt tcc ttc act tca gat cgt gca tct gat ggc agg gat gac gaa gcc 96
 Val Ser Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala
 15 20 25 30
 aaa gac gaa agg tct gac atg cac gaa tcg gac cgg aaa gga cgc gca 144
 Lys Asp Glu Arg Ser Asp Met His Glu Ser Asp Arg Lys Gly Arg Ala
 35 40 45
 tac tgt tgc cat cct gtc tgt ggc aaa aac ttt gat tgt gga cgc 189
 Tyr Cys Cys His Pro Val Cys Gly Lys Asn Phe Asp Cys Gly Arg
 50 55 60
 tgatgctcca ggaccctctg aaccacgacc tcgag 224

<210> 386
 <211> 61

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<210> 392
 <211> 63
 <212> PRT
 <213> Conus arenatus

<400> 392
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Asp Ser
 1 5 10 15
 Phe Thr Pro Val Arg Thr Ser Val Gly Arg Ser Ala Ala Ala Asn Ala
 20 25 30
 Phe Asp Arg Ile Ala Leu Thr Ala Arg Gln Asp Tyr Cys Cys Thr Ile
 35 40 45
 Pro Ser Cys Trp Asp Arg Tyr Lys Glu Arg Cys Arg His Ile Arg
 50 55 60

<210> 393
 <211> 22
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 16 is Glu or
 gamma-carboxy-Glu; Xaa at residue 8 is Pro or hydroxy-Pro; Xaa at
 residue 11 is Trp (D or L) or bromo-Trp (D or L);
 <220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residues 3 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo
 -Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 393
 Xaa Asp Xaa Cys Cys Thr Ile Xaa Ser Cys Xaa Asp Arg Xaa Lys Xaa
 1 5 10 15
 Arg Cys Arg His Ile Arg
 20

<210> 394
 <211> 230
 <212> DNA
 <213> Conus eburneus

<220>
 <221> CDS
 <222> (7)..(195)

<400> 394
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtg 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10
 gat tcc ttc act tca gtt cgt act tcc gtt ggc agg agt gct gca gcc 96
 Asp Ser Phe Thr Ser Val Arg Thr Ser Val Gly Arg Ser Ala Ala Ala
 15 20 25 30
 aac gcg ttt gac cgg atc gct ctg acc gcc agg caa gat tat tgc tgt 144
 Asn Ala Phe Asp Arg Ile Ala Leu Thr Ala Arg Gln Asp Tyr Cys Cys
 35 40 45

Leu Pro Val Thr Leu Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala
 15 20 25 30
 aac gcc aaa acg cct cgc ctg atc gcg cca ttc atc agg gat tat tgc 144
 Asn Ala Lys Thr Pro Arg Leu Ile Ala Pro Phe Ile Arg Asp Tyr Cys
 35 40 45
 tgt cat aga ggt ccc tgt atg gta tgg tgt ggt tgaagccgct gctgctccag 197
 Cys His Arg Gly Pro Cys Met Val Trp Cys Gly
 50 55
 gaccctctga accacgacct cgag 221
 <210> 398
 <211> 57
 <212> PRT
 <213> Conus miles
 <400> 398
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ala Val Leu Pro
 1 5 10 15
 Val Thr Leu Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala
 20 25 30
 Lys Thr Pro Arg Leu Ile Ala Pro Phe Ile Arg Asp Tyr Cys Cys His
 35 40 45
 Arg Gly Pro Cys Met Val Trp Cys Gly
 50 55
 <210> 399
 <211> 13
 <212> PRT
 <213> Conus miles
 <220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 8 is Pro or hydroxy-Pro; Xaa at residue 12 is Trp
 (D or L) or bromo-Trp (D or L); Xaa at residue 2 is Tyr, 125I-Tyr
 , mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
 <400> 399
 Asp Xaa Cys Cys His Arg Gly Xaa Cys Met Val Xaa Cys
 1 5 10
 <210> 400
 <211> 218
 <212> DNA
 <213> Conus jDedius
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 <222> (7)..(174)
 <400> 400
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10
 gtt tcc aac tct tca gat cgt ggt cca gca tct aat aaa agg aag aat 96
 Val Ser Asn Ser Ser Asp Arg Gly Pro Ala Ser Asn Lys Arg Lys Asn
 15 20 25 30

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gcc gca atg ctt gac atg atc gct caa cac gcc ata agg ggt tgc tgt 144
Ala Ala Met Leu Asp Met Ile Ala Gln His Ala Ile Arg Gly Cys Cys
35 40 45

tcc gat cct cgc tgt aga tat aga tgt cgt tgaagacgct gctgctccag 194
Ser Asp Pro Arg Cys Arg Tyr Arg Cys Arg
50 55

gaccctctga accacgacct cgag 218

<210> 401
<211> 56
<212> PRT
<213> Conus jDedius

<400> 401
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15
Asn Ser Ser Asp Arg Gly Pro Ala Ser Asn Lys Arg Lys Asn Ala Ala
20 25 30

Met Leu Asp Met Ile Ala Gln His Ala Ile Arg Gly Cys Cys Ser Asp
35 40 45

Pro Arg Cys Arg Tyr Arg Cys Arg
50 55

<210> 402
<211> 13
<212> PRT
<213> Conus jDedius

<220>
<221> PEPTIDE
<222> (1)..(13)
<223> Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at residue 10 is Tyr,
125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 402
Gly Cys Cys Ser Asp Xaa Arg Cys Arg Xaa Arg Cys Arg
1 5 10

<210> 403
<211> 17
<212> PRT
<213> Conus omaria

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro

<400> 403
Gly Cys Cys Ser His Xaa Ala Cys Asn Val Asn Asn Xaa His Ile Cys
1 5 10 15

Gly

<210> 404
<211> 17
<212> PRT
<213> Conus omaria

<220>

10072692-00102

<221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro; C terminus contains free hydroxyl

<400> 404
 Gly Cys Cys Ser His Xaa Ala Cys Asn Val Asn Asn Xaa His Ile Cys
 1 5 10 15

Gly

<210> 405
 <211> 224
 <212> DNA
 <213> Conus quercinus

<220>
 <221> CDS
 <222> (7)..(189)

<400> 405
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 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10

act tca gat cgt gta tct aat ggc agg aaa gct gca gcc aaa ttc aaa 96
 Thr Ser Asp Arg Val Ser Asn Gly Arg Lys Ala Ala Ala Lys Phe Lys
 15 20 25 30

gcg cct gcc ctg atg gag ctg tcc gtc agg caa gga tgc tgt tca gat 144
 Ala Pro Ala Leu Met Glu Leu Ser Val Arg Gln Gly Cys Cys Ser Asp
 35 40 45

cct gcc tgt gcc gtg agc aat cca gac atc tgt ggc gga gga cgc 189
 Pro Ala Cys Ala Val Ser Asn Pro Asp Ile Cys Gly Gly Gly Arg
 50 55 60

tgatgctcca ggaccctctg aaccacgacc tcgag 224

<210> 406
 <211> 61
 <212> PRT
 <213> Conus quercinus

<400> 406
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Thr Ser
 1 5 10 15

Asp Arg Val Ser Asn Gly Arg Lys Ala Ala Ala Lys Phe Lys Ala Pro
 20 25 30

Ala Leu Met Glu Leu Ser Val Arg Gln Gly Cys Cys Ser Asp Pro Ala
 35 40 45

Cys Ala Val Ser Asn Pro Asp Ile Cys Gly Gly Gly Arg
 50 55 60

<210> 407
 <211> 19
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(19)

1007550000

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 7 and 14 is Pro or hydroxy-Pro

<400> 407

Xaa Gly Cys Cys Ser Asp Xaa Ala Cys Ala Val Ser Asn Xaa Asp Ile
1 5 10 15

Cys Gly Gly

<210> 408

<211> 230

<212> DNA

<213> Conus bandanus

<220>

<221> CDS

<222> (7)..(186)

<400> 408

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtt 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
1 5 10

gtt tcc ttc act tca aat cgt gca ttt cgt cgt agg aat gcc gta gcc 96
Val Ser Phe Thr Ser Asn Arg Ala Phe Arg Arg Arg Asn Ala Val Ala
15 20 25 30

aaa gcg tct gac ctg atc gct ctg aac gcc agg aga cca gaa tgc tgt 144
Lys Ala Ser Asp Leu Ile Ala Leu Asn Ala Arg Arg Pro Glu Cys Cys
35 40 45

act cat cct gcc tgt cac gtg agt cat cca gaa ctc tgt ggt 186
Thr His Pro Ala Cys His Val Ser His Pro Glu Leu Cys Gly
50 55 60

tgaagacgct gacgctccag gaccctctga accacgacct cgag 230

<210> 409

<211> 60

<212> PRT

<213> Conus bandanus

<400> 409

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Phe Thr Ser Asn Arg Ala Phe Arg Arg Arg Asn Ala Val Ala Lys Ala
20 25 30

Ser Asp Leu Ile Ala Leu Asn Ala Arg Arg Pro Glu Cys Cys Thr His
35 40 45

Pro Ala Cys His Val Ser His Pro Glu Leu Cys Gly
50 55 60

<210> 410

<211> 17

<212> PRT

<213> Conus bandanus

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residues 2 and 15 is Glu or gamma-carboxy-Glu; Xaa at residues 1, 7 and 14 is Pro or hydroxy-Pro

<400> 413
 Xaa Xaa Cys Cys Thr His Xaa Ala Cys His Val Ser Asn Xaa Xaa Leu
 1 5 10 15

Cys

<210> 414
 <211> 218
 <212> DNA
 <213> Conus miles

<220>
 <221> CDS
 <222> (7)..(174)

<400> 414
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 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10

gtt tcc gtc act tca tat cgt gca tct cat ggc agg aag gac gca gcc 96
 Val Ser Val Thr Ser Tyr Arg Ala Ser His Gly Arg Lys Asp Ala Ala
 15 20 25 30

gac ctg agc gct ctg aac gac aac aat aat tgc tgt aac cat cct gcc 144
 Asp Leu Ser Ala Leu Asn Asp Asn Asn Asn Cys Cys Asn His Pro Ala
 35 40 45

.tgt gcc ggg aaa aat tca gat ctt tgt ggt tgaagacgct gctgctccag 194
 Cys Ala Gly Lys Asn Ser Asp Leu Cys Gly
 50 55

gaccctctga accacgacct cgag 218

<210> 415
 <211> 56
 <212> PRT
 <213> Conus miles

<400> 415
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Val Thr Ser Tyr Arg Ala Ser His Gly Arg Lys Asp Ala Ala Asp Leu
 20 25 30

Ser Ala Leu Asn Asp Asn Asn Asn Cys Cys Asn His Pro Ala Cys Ala
 35 40 45

Gly Lys Asn Ser Asp Leu Cys Gly
 50 55

<210> 416
 <211> 15
 <212> PRT
 <213> Conus miles

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 5 is Pro or hydroxy-Pro

<400> 416
 Cys Cys Asn His Xaa Ala Cys Ala Gly Lys Asn Ser Asp Leu Cys
 1 5 10 15

10072603446

Lys Val Ser Asp Met Ile Ala Leu Thr Ala Arg Arg Thr Cys Cys Ser

35 40 45

Arg Pro Thr Cys Arg Met Glu Tyr Pro Glu Leu Cys Gly Gly Arg Arg
50 55 60

<210> 423
<211> 17
<212> PRT
<213> Conus atlanticus

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residues 11 and 14 is Glu or gamma-carboxy-Glu; Xaa at residues 6 and 13 is Pro or hydroxy-Pro; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 423
Thr Cys Cys Ser Arg Xaa Thr Cys Arg Met Xaa Xaa Xaa Xaa Leu Cys
1 5 10 15

Gly

<210> 424
<211> 227
<212> DNA
<213> Conus quercinus

<220>
<221> CDS
<222> (7)..(192)

<220>
<221> misc_feature
<222> (1)..(227)
<223> n is unknown

<400> 424
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca atc acg gtg 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Ile Thr Val
1 5 10

gtt tcc ttc acc tca gat cat gca tct gat ggc agg aat acc gca gcc 96
Val Ser Phe Thr Ser Asp His Ala Ser Asp Gly Arg Asn Thr Ala Ala
15 20 25 30

aac gac aaa gcg tct aaa ctg atg gct ctt acg aac gaa tgc tgt gac 144
Asn Asp Lys Ala Ser Lys Leu Met Ala Leu Thr Asn Glu Cys Cys Asp
35 40 45

aat cct ccg tgc aag tcg agt aat cca gat ttg tgt gac tgg aga agc 192
Asn Pro Pro Cys Lys Ser Ser Asn Pro Asp Leu Cys Asp Trp Arg Ser
50 55 60

tgatgctcca ggaccctntg aaccacgacc tcgag 227

<210> 425
<211> 62
<212> PRT
<213> Conus quercinus

<400> 425
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Ile Thr Val Val Ser
1 5 10 15

10072203-2215

Phe Thr Ser Asp His Ala Ser Asp Gly Arg Asn Thr Ala Ala Asn Asp
20 25 30

Lys Ala Ser Lys Leu Met Ala Leu Thr Asn Glu Cys Cys Asp Asn Pro
35 40 45

Pro Cys Lys Ser Ser Asn Pro Asp Leu Cys Asp Trp Arg Ser
50 55 60

<210> 426

<211> 21

<212> PRT

<213> Conus quercinus

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> Xaa at residue 2 is Glu or gamma-carboxy-Glu; Xaa at residues 7,
8 and 14 is Pro or hydroxy-Pro; Xaa at residue 19 is Trp (D or L)
or bromo-Trp (D or L)

<400> 426

Asn Xaa Cys Cys Asp Asn Xaa Xaa Cys Lys Ser Ser Asn Xaa Asp Leu
1 5 10 15

Cys Asp Xaa Arg Ser
20

<210> 427

<211> 221

<212> DNA

<213> Conus leopardus

<220>

<221> CDS

<222> (7)..(177)

<400> 427

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acg gtc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
1 5 10

gtt tcc ctc act tta gat cgt gca tct ggt ggc agg aga tct gga gcc 96
Val Ser Leu Thr Leu Asp Arg Ala Ser Gly Gly Arg Arg Ser Gly Ala
15 20 25 30

gac aac atg att gct ctt ctg atc atc aga aaa tgc tgt tcc aat ccc 144
Asp Asn Met Ile Ala Leu Leu Ile Ile Arg Lys Cys Cys Ser Asn Pro
35 40 45

gcc tgt aac agg tat aat cca gca att tgt gat tgaagacgct aatgctccag 197
Ala Cys Asn Arg Tyr Asn Pro Ala Ile Cys Asp
50 55

gaccctctga accacgacct cgag 221

<210> 428

<211> 57

<212> PRT

<213> Conus leopardus

<400> 428

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1 5 10 15

Leu Thr Leu Asp Arg Ala Ser Gly Gly Arg Arg Ser Gly Ala Asp Asn
 20 25 30

Met Ile Ala Leu Leu Ile Ile Arg Lys Cys Cys Ser Asn Pro Ala Cys
 35 40 45

Asn Arg Tyr Asn Pro Ala Ile Cys Asp
 50 55

<210> 429

<211> 16

<212> PRT

<213> Conus leopardus

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residues 5 and 12 is Pro or hydroxy-Pro; Xaa at residue 10
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
 phospho-Tyr

<400> 429

Cys Cys Ser Asn Xaa Ala Cys Asn Arg Xaa Asn Xaa Ala Ile Cys Asp
 1 5 10 15

<210> 430

<211> 224

<212> DNA

<213> Conus emaciatatus

<220>

<221> CDS

<222> (7)..(180)

<400> 430

ggatcc atg ttc acc gtg ttt ctg ttg gtt ctc ttg gca acc act gtc 48
 Met Phe Thr Val Phe Leu Leu Val Leu Ala Thr Thr Val
 1 5 10

act tta cat cgt gca tct aat ggc agg aat gcc gca gcc agc agg aaa 96
 Thr Leu His Arg Ala Ser Asn Gly Arg Asn Ala Ala Ala Ser Arg Lys
 15 20 25 30

gcg tct gcc ctg atc gct cag atc gcc ggt aga gac tgc tgt aac ttt 144
 Ala Ser Ala Leu Ile Ala Gln Ile Ala Gly Arg Asp Cys Cys Asn Phe
 35 40 45

cct gct tgt gcc gcg agt aat cca ggc ctt tgt act tgaagacgct 190
 Pro Ala Cys Ala Ala Ser Asn Pro Gly Leu Cys Thr
 50 55

gctgctccag gaccctctga accacgacct cgag 224

<210> 431

<211> 58

<212> PRT

<213> Conus emaciatatus

<400> 431

Met Phe Thr Val Phe Leu Leu Val Leu Leu Ala Thr Thr Val Thr Leu
 1 5 10 15

His Arg Ala Ser Asn Gly Arg Asn Ala Ala Ala Ser Arg Lys Ala Ser
 20 25 30

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

Ala Leu Ile Ala Gln Ile Ala Gly Arg Asp Cys Cys Asn Phe Pro Ala
35 40 45

Cys Ala Ala Ser Asn Pro Gly Leu Cys Thr
50 55

<210> 432
<211> 17
<212> PRT
<213> Conus emaciatus

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro

<400> 432
Asp Cys Cys Asn Phe Xaa Ala Cys Ala Ala Ser Asn Xaa Gly Leu Cys
1 5 10 15

Thr

<210> 433
<211> 215
<212> DNA
<213> Conus victor

<220>
<221> CDS
<222> (7)..(180)

<400> 433
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc atc 48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Ile
1 5 10

gtt tcc tcc act tta gat cgt gca tct gat ggc atg aat gct gca gcg 96
Val Ser Ser Thr Leu Asp Arg Ala Ser Asp Gly Met Asn Ala Ala Ala
15 20 25 30
tct gac ctg atc gct ctg agc atc agg aga tgc tgt tct tct cct ccc 144
Ser Asp Leu Ile Ala Leu Ser Ile Arg Arg Cys Cys Ser Ser Pro Pro
35 40 45

tgt ttc gcg agt aat cca gct tgt ggt aga cga cgc tgatgctcca 190
Cys Phe Ala Ser Asn Pro Ala Cys Gly Arg Arg Arg
50 55

ggaccctctg aaccacgacc tcgag 215

<210> 434
<211> 58
<212> PRT
<213> Conus victor

<400> 434
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Ile Val Ser
1 5 10 15

Ser Thr Leu Asp Arg Ala Ser Asp Gly Met Asn Ala Ala Ala Ser Asp
20 25 30

Leu Ile Ala Leu Ser Ile Arg Arg Cys Cys Ser Ser Pro Pro Cys Phe
35 40 45

Ala Ser Asn Pro Ala Cys Gly Arg Arg Arg

10072603-03440

50 55

<210> 435
 <211> 14
 <212> PRT
 <213> Conus victor

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residues 5, 6 and 13 is Pro or hydroxy-Pro

<400> 435
 Cys Cys Ser Ser Xaa Xaa Cys Phe Ala Ser Asn Xaa Ala Cys
 1 5 10

<210> 436
 <211> 230
 <212> DNA
 <213> Conus cinereus gubba

<220>
 <221> CDS
 <222> (7)..(195)

<400> 436
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ctg gca acc act atc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Ile
 1 5 10

gtt tcc tcc act tca ggt cat gca ttt gat ggc agg aat gct gca gcc 96
 Val Ser Ser Thr Ser Gly His Ala Phe Asp Gly Arg Asn Ala Ala Ala
 15 20 25 30

gac tac aaa ggg tct gaa ttg ctt gct atg acc gtc agg gga gga tgc 144
 Asp Tyr Lys Gly Ser Glu Leu Leu Ala Met Thr Val Arg Gly Gly Cys
 35 40 45

tgt tcc ttt cct ccc tgt atc gca aat aat cct ttt tgt gct gga aga 192
 Cys Ser Phe Pro Pro Cys Ile Ala Asn Asn Pro Phe Cys Ala Gly Arg
 50 55 60

cgc tgatgctcca ggaccctctg aaccacgacc tcgag 230
 Arg

<210> 437
 <211> 63
 <212> PRT
 <213> Conus cinereus gubba

<400> 437
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Ile Val Ser
 1 5 10 15

Ser Thr Ser Gly His Ala Phe Asp Gly Arg Asn Ala Ala Ala Asp Tyr
 20 25 30

Lys Gly Ser Glu Leu Leu Ala Met Thr Val Arg Gly Gly Cys Cys Ser
 35 40 45

Phe Pro Pro Cys Ile Ala Asn Asn Pro Phe Cys Ala Gly Arg Arg
 50 55 60

<210> 438
 <211> 17

10072500-03100

<212> PRT
 <213> Conus cinereus gubba

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residues 7, 8 and 14 is Pro or hydroxy-Pro

<400> 438
 Gly Gly Cys Cys Ser Phe Xaa Xaa Cys Ile Ala Asn Asn Xaa Phe Cys
 1 5 10 15

Ala

<210> 439
 <211> 221
 <212> DNA
 <213> Conus flavidus

<220>
 <221> CDS
 <222> (7)..(177)

<400> 439
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttc gca tcc tct gtc 48
 Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val
 1 5 10

act tta gat cgt gca tct cat ggc agg tat atc cca gtc gtc gac aga 96
 Thr Leu Asp Arg Ala Ser His Gly Arg Tyr Ile Pro Val Val Asp Arg
 15 20 25 30
 gcg tct gcc ctg atg gct cag gcc gac ctt aga ggt tgc tgt tcc aat 144
 Ala Ser Ala Leu Met Ala Gln Ala Asp Leu Arg Gly Cys Cys Ser Asn
 35 40 45

cct cct tgt tcc tat ctt aat cca gcc tgt ggt taaagacgct gccgctccag 197
 Pro Pro Cys Ser Tyr Leu Asn Pro Ala Cys Gly
 50 55

gaccctctga accacgacct cgag 221

<210> 440
 <211> 57
 <212> PRT
 <213> Conus flavidus

<400> 440
 Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val Thr Leu
 1 5 10 15

Asp Arg Ala Ser His Gly Arg Tyr Ile Pro Val Val Asp Arg Ala Ser
 20 25 30

Ala Leu Met Ala Gln Ala Asp Leu Arg Gly Cys Cys Ser Asn Pro Pro
 35 40 45

Cys Ser Tyr Leu Asn Pro Ala Cys Gly
 50 55

<210> 441
 <211> 15
 <212> PRT
 <213> Conus flavidus

<220>

20250320100000

<221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro; Xaa at residue 10 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 441
 Gly Cys Cys Ser Asn Xaa Xaa Cys Ser Xaa Leu Asn Xaa Ala Cys
 1 5 10 15

<210> 442
 <211> 221
 <212> DNA
 <213> Conus emaciatus

<220>
 <221> CDS
 <222> (7)..(177)

<400> 442
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttc gca tcc tct gtc 48
 Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val
 1 5 10

act tta gat cgt gca tct cat ggc agg tat gcc gca gtc gtc aac aga 96
 Thr Leu Asp Arg Ala Ser His Gly Arg Tyr Ala Ala Val Val Asn Arg
 15 20 25 30
 gcg tct gcc ctg atg gct cat gcc gcc ctt cga gat tgc tgt tcc gat 144
 Ala Ser Ala Leu Met Ala His Ala Ala Leu Arg Asp Cys Cys Ser Asp
 35 40 45

cct cct tgt gct cat aat aat cca gac tgt cgt taaagacgct gctgctccag 197
 Pro Pro Cys Ala His Asn Asn Pro Asp Cys Arg
 50 55

gaccctctga accacgacct cgag 221

<210> 443
 <211> 57
 <212> PRT
 <213> Conus emaciatus

<400> 443
 Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val Thr Leu
 1 5 10 15

Asp Arg Ala Ser His Gly Arg Tyr Ala Ala Val Val Asn Arg Ala Ser
 20 25 30

Ala Leu Met Ala His Ala Ala Leu Arg Asp Cys Cys Ser Asp Pro Pro
 35 40 45

Cys Ala His Asn Asn Pro Asp Cys Arg
 50 55

<210> 444
 <211> 16
 <212> PRT
 <213> Conus emaciatus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro

100720022002

<400> 444
 Asp Cys Cys Ser Asp Xaa Xaa Cys Ala His Asn Asn Xaa Asp Cys Arg
 1 5 10 15

<210> 445
 <211> 230
 <212> DNA
 <213> Conus generalis

<220>
 <221> CDS
 <222> (7)..(195)

<400> 445
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca act act gtc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10

gtt tcc ttc act tca gat cgt ggg tct gat ggc agg aat gcc gca gcc 96
 Val Ser Phe Thr Ser Asp Arg Gly Ser Asp Gly Arg Asn Ala Ala Ala
 15 20 25 30

aag gac aaa gcg tct gac ctg gtc gct ctg acc gtc aag gga tgc tgt 144
 Lys Asp Lys Ala Ser Asp Leu Val Ala Leu Thr Val Lys Gly Cys Cys
 35 40 45

tct aat cct ccc tgt tac gcg aat aat caa gcc tat tgt aat gga aga 192
 Ser Asn Pro Pro Cys Tyr Ala Asn Asn Gln Ala Tyr Cys Asn Gly Arg
 50 55 60

cgc tgatgctcca ggaccctctg aaccacgacc tcgag 230
 Arg

<210> 446
 <211> 63
 <212> PRT
 <213> Conus generalis

<400> 446
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Phe Thr Ser Asp Arg Gly Ser Asp Gly Arg Asn Ala Ala Ala Lys Asp
 20 25 30

Lys Ala Ser Asp Leu Val Ala Leu Thr Val Lys Gly Cys Cys Ser Asn
 35 40 45

Pro Pro Cys Tyr Ala Asn Asn Gln Ala Tyr Cys Asn Gly Arg Arg
 50 55 60

<210> 447
 <211> 17
 <212> PRT
 <213> Conus generalis

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residues 6 and 7 is Pro or hydroxy-Pro; Xaa at residues 9
 and 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 447
 Gly Cys Cys Ser Asn Xaa Xaa Cys Xaa Ala Asn Asn Gln Ala Xaa Cys

1 5 10 15

Asn

<210> 448
 <211> 212
 <212> DNA
 <213> Conus wittigi

<220>
 <221> CDS
 <222> (7)..(195)

<400> 448
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ctg gca acc act gtc 48
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
 1 5 10

gtt tcc ccc act aga gat cgt gca tct ggt gtc agg aat gtt gtt gca 96
 Val Ser Pro Thr Arg Asp Arg Ala Ser Gly Val Arg Asn Val Val Ala
 15 20 25 30

aca agc ttt cag act ctg acc cac gat gaa tgc tgt gca cac cct tcc 144
 Thr Ser Phe Gln Thr Leu Thr His Asp Glu Cys Cys Ala His Pro Ser
 35 40 45

tgt tgg aag gcc gaa gac ctg att tgt act aat caa cgt cgc agg acc 192
 Cys Trp Lys Ala Glu Asp Leu Ile Cys Thr Asn Gln Arg Arg Arg Thr
 50 55 60

ctc tgaaccacga cctcgag 212
 Leu

<210> 449
 <211> 63
 <212> PRT
 <213> Conus wittigi

<400> 449
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
 1 5 10 15

Pro Thr Arg Asp Arg Ala Ser Gly Val Arg Asn Val Val Ala Thr Ser
 20 25 30

Phe Gln Thr Leu Thr His Asp Glu Cys Cys Ala His Pro Ser Cys Trp
 35 40 45

Lys Ala Glu Asp Leu Ile Cys Thr Asn Gln Arg Arg Arg Thr Leu
 50 55 60

<210> 450
 <211> 25

<212> PRT

<213> Conus wittigi

<220>

<221> PEPTIDE

<222> (1)..(25)

164-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000

<213> Conus characteristicus

<220>

<221> PEPTIDE

<222> (1)..(20)

<223> Xaa at residue 7 is Glu or gamma-carboxy-Glu; Xaa at residue 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 453

Gly Cys Cys Ala Ile Arg Xaa Cys Arg Leu Gln Asn Ala Ala Xaa Cys
1 5 10 15

Gly Gly Ile Ser
20

<210> 454

<211> 568

<212> DNA

<213> Conus betulinus

<220>

<221> CDS

<222> (395)..(508)

<220>

<221> misc_feature

<222> (1)..(568)

<223> n is unknown

<400> 454

agtaattnat atannagaaa gnaananaaa annatanaga atttaagtaa tntaagaann 60

gaganagtga atagnagnta agtagannaa ganaggtaga nagnanangn ggangntagn 120

taatagatan nntatngaga nttantagc ngtatanana agaaaagagg gnaanngaaa 180

tgngngaann ataantanta nngatngann ngnaagtgnn aagngtanaa ggaanaacaa 240

antngttgtn taatntgnnt gngtgtgtnt gtgtgngtgt gtgtgtgtgn gtgngtgtgt 300

ntgtgngnnt gtgtgngngn gngngtgtgt gtgtgngtgt gtgtgtgtgt gtgtgtgtgt 360

gtgtgtgtgt gngtgtgtgg ttctggatcc agca tct ggt ggc agg aag gct gca 415
Ser Gly Gly Arg Lys Ala Ala
1 5

gcc aaa gcg tct aac cgg atc gct ctg acc gtc agg agt gca aca tgc 463
Ala Lys Ala Ser Asn Arg Ile Ala Leu Thr Val Arg Ser Ala Thr Cys
10 15 20

tgt tat tat cct ccc tgt tac gag gct tat cca gaa agt tgt ctg 508
Cys Tyr Tyr Pro Pro Cys Tyr Glu Ala Tyr Pro Glu Ser Cys Leu
25 30 35

taacgtgaat catccagacc tttgtggctg aagaccctga tgctccaggg gcaagttcaa 568

<210> 455

<211> 38

<212> PRT

<213> Conus betulinus

<400> 455

Ser Gly Gly Arg Lys Ala Ala Ala Lys Ala Ser Asn Arg Ile Ala Leu
1 5 10 15

Thr Val Arg Ser Ala Thr Cys Cys Tyr Tyr Pro Pro Cys Tyr Glu Ala
 20 25 30

Tyr Pro Glu Ser Cys Leu
 35

<210> 456
 <211> 19
 <212> PRT
 <213> Conus betulinus

<220>
 <221> PEPTIDE
 <222> (1)..(19)
 <223> Xaa at residues 12 and 16 is Glu or gamma-carboxy-Glu; Xaa at residues 8, 9 and 13 is Pro or hydroxy-Pro; Xaa at residues 6, 7, 11 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 456
 Ser Ala Thr Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Ala Xaa Xaa Xaa
 1 5 10 15

Ser Cys Leu

<210> 457
 <211> 29
 <212> PRT
 <213> Conus textile

<400> 457
 Asp Cys Arg Gly Tyr Asp Ala Pro Cys Ser Ser Gly Ala Pro Cys Cys
 1 5 10 15

Asp Trp Trp Thr Cys Ser Ala Arg Thr Asn Arg Cys Phe
 20 25

<210> 458
 <211> 31
 <212> PRT
 <213> Conus ammiralis

<400> 458
 Gly Met Trp Gly Asp Cys Lys Asp Gly Leu Thr Thr Cys Phe Ala Pro
 1 5 10 15

Ser Glu Cys Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp
 20 25 30

<210> 459
 <211> 36
 <212> PRT
 <213> Conus ammiralis

<400> 459
 Trp Arg Glu Gly Ser Cys Thr Ser Trp Leu Ala Thr Cys Thr Gln Asp
 1 5 10 15

Gln Gln Cys Cys Thr Asp Val Cys Tyr Lys Arg Asp Tyr Cys Ala Leu
 20 25 30

Trp Asp Asp Arg
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Conus betulinus

<212> PRT
 <213> *Conus pennaceus*

<220>
 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residues 14 and 26 is gamma-carboxy-Glu; Xaa at residue 31
 is hydroxy-Pro

<400> 465
 Asp Cys Thr Ser Trp Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys
 1 5 10 15
 Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser
 20 25 30

<210> 466
 <211> 32
 <212> PRT
 <213> *Conus gloriamaris*

<400> 466
 Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser Pro Gly Ala Gln Cys Cys
 1 5 10 15
 Ser Leu Leu Met Cys Ser Lys Ala Thr Ser Arg Cys Ile Leu Ala Leu
 20 25 30

<210> 467
 <211> 27
 <212> PRT
 <213> *Conus textile*

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa is gamma-carboxy-Glu

<400> 467
 Cys Lys Thr Tyr Ser Lys Tyr Cys Xaa Ala Asp Ser Xaa Cys Cys Thr
 1 5 10 15
 Xaa Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe
 20 25

<210> 468
 <211> 29
 <212> PRT
 <213> *Conus marmoreus*

<220>
 <221> PEPTIDE
 <222> (1)..(29)
 <223> Xaa is gamma-carboxy-Glu

<400> 468
 Asn Gly Gln Cys Glu Asp Val Trp Met Pro Cys Thr Ser Asn Trp Xaa
 1 5 10 15
 Cys Cys Ser Leu Asp Cys Glu Met Tyr Cys Thr Gln Ile
 20 25

<210> 469
 <211> 27
 <212> PRT

<213> *Conus marmoreus*

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa is gamma-carboxy-Glu

<400> 469

Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Xaa Cys Cys Ser
1 5 10 15

Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe
20 25

<210> 470

<211> 26

<212> PRT

<213> *Conus marmoreus*

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa is gamma-carboxy-Glu

<400> 470

Asn Gly Gly Cys Lys Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Xaa
1 5 10 15

Cys Cys Ser Met Ser Cys Asp Met Tyr Cys
20 25

<210> 471

<211> 33

<212> PRT

<213> *Conus radiatus*

<220>

<221> PEPTIDE

<222> (1)..(33)

<223> Xaa at residues 1, 10 and 33 is bromo-Trp; Xaa at residues 5, 6, 15 and 26 is gamma-carboxy-Glu

<400> 471

Xaa Phe Gly His Xaa Xaa Cys Thr Tyr Xaa Leu Gly Pro Cys Xaa Val
1 5 10 15

Asp Asp Thr Cys Cys Ser Ala Ser Cys Xaa Ser Lys Phe Cys Gly Leu
20 25 30

Xaa

<210> 472

<211> 31

<212> PRT

<213> *Conus radiatus*

<400> 472

Trp Trp Glu Gly Glu Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro
1 5 10 15

Ser Asn Cys Cys Leu Lys Ser Cys Asn Gly His Cys Thr Leu Trp
20 25 30

<210> 473

<211> 26

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<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residues 3 and 8 is hydroxy-Pro; Xaa at residues 7 and 14
is gamma-carboxy-Glu

<400> 473
Leu Cys Xaa Asp Tyr Thr Xaa Xaa Cys Ser His Ala His Xaa Cys Cys
1 5 10 15
Ser Trp Asn Cys Tyr Asn Gly His Cys Thr
20 25

<210> 474
<211> 28
<212> PRT
<213> Conus textile

<400> 474
Asp Cys Tyr Ser Trp Leu Gly Ser Cys Ile Ala Pro Ser Gln Cys Cys
1 5 10 15
Ser Glu Val Cys Asp Tyr Tyr Cys Arg Leu Trp Arg
20 25

<210> 475
<211> 34
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(34)
<223> Xaa is gamma-carboxy-Glu

<400> 475
Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser Xaa
1 5 10 15
Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro Pro
20 25 30

Asp Trp

<210> 476
<211> 31
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(31)
<223> Xaa is gamma-carboxy-Glu

<400> 476
Gly Met Trp Gly Glu Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro
1 5 10 15
Ser Xaa Cys Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp
20 25 30

<210> 477

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20 25 30
 His Phe Tyr Arg Gly Cys Thr Cys Ser Cys Gln
 35 40
 <210> 481
 <211> 42
 <212> PRT
 <213> Conus characteristicus
 <400> 481
 Gly Cys Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly
 1 5 10 15
 Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His
 20 25 30
 His Phe Tyr Arg Gly Cys Thr Cys Thr Cys
 35 40
 <210> 482
 <211> 42
 <212> PRT
 <213> Conus characteristicus
 <400> 482
 Gly Cys Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly
 1 5 10 15
 Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His
 20 25 30
 His Phe Tyr Arg Gly Cys Thr Cys Thr Cys
 35 40
 <210> 483
 <211> 42
 <212> PRT
 <213> Conus characteristicus
 <400> 483
 Gly Cys Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly
 1 5 10 15
 Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His
 20 25 30
 His Phe Tyr Arg Gly Cys Thr Cys Thr Cys
 35 40
 <210> 484
 <211> 42
 <212> PRT
 <213> Conus characteristicus
 <400> 484
 Gly Cys Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly
 1 5 10 15
 Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His
 20 25 30
 His Phe Tyr Arg Gly Cys Thr Cys Thr Cys
 35 40

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<400> 489
 Lys Cys Asn Phe Asp Lys Cys Lys Gly Thr Gly Val Tyr Asn Cys Gly
 1 5 10 15
 Glu Ser Cys Ser Cys Glu Gly Leu His Ser Cys Arg Cys Thr Tyr Asn
 20 25 30
 Ile Gly Ser Met Lys Ser Gly Cys Ala Cys Ile Cys Thr Tyr Tyr
 35 40 45

<210> 490
 <211> 44
 <212> PRT
 <213> Conus radiatus

<400> 490
 Tyr Gly Leu Gly Cys Ala Gly Thr Cys Gly Ser Ser Ser Asn Cys Val
 1 5 10 15
 Arg Asp Tyr Cys Asp Cys Pro Lys Pro Asn Cys Tyr Cys Thr Gly Lys
 20 25 30
 Gly Phe Arg Gln Pro Gly Cys Gly Cys Ser Cys Leu
 35 40

<210> 491
 <211> 46
 <212> PRT
 <213> Conus striolatus

<400> 491
 Gln Cys Thr Phe Val Asn Asn Cys Gln Gln Asn Gly Cys Ala Asn Gly
 1 5 10 15
 Asp Cys Ser Cys Gly Asp Gln Ile Cys Lys Cys Gly Tyr Arg Ile Ser
 20 25 30
 Pro Gly Arg Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys
 35 40 45

<210> 492
 <211> 44
 <212> PRT
 <213> Conus tulipa

<400> 492
 Phe Gly Pro Ile Cys Thr Cys Phe Lys Ser Gln Asn Cys Arg Gly Ser
 1 5 10 15
 Cys Glu Cys Met Ser Pro Pro Gly Cys Tyr Cys Ser Asn Asn Gly Ile
 20 25 30
 Arg Glu Arg Gly Cys Ser Cys Thr Cys Pro Gly Thr
 35 40

<210> 493
 <211> 46
 <212> PRT
 <213> Conus tulipa

<400> 493
 Gly Cys Thr Gly Asn Cys Asp Trp Thr Cys Ser Gly Asp Cys Ser Cys
 1 5 10 15
 Gln Gly Thr Ser Asp Ser Cys His Cys Ile Pro Pro Lys Ser Ile Gly
 20 25 30

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<400> 500

Gly Cys Cys Ala Met Leu Thr Cys Cys Val
1 5 10

<210> 501

<211> 12

<212> PRT

<213> Conus purpurascens

<400> 501

Gly Cys Cys Pro Lys Gln Met Arg Cys Cys Thr Leu
1 5 10

<210> 502

<211> 11

<212> PRT

<213> Conus characteristicus

<400> 502

Cys Cys Pro Arg Arg Leu Ala Cys Cys Ile Ile
1 5 10

<210> 503

<211> 10

<212> PRT

<213> Conus characteristicus

<400> 503

Cys Cys Pro Asn Lys Pro Cys Cys Phe Ile
1 5 10

<210> 504

<211> 13

<212> PRT

<213> Conus geographus

<400> 504

Glx Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Ile
1 5 10

<210> 505

<211> 13

<212> PRT

<213> Conus geographus

<400> 505

Glx Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Val
1 5 10

<210> 506

<211> 15

<212> PRT

<213> Conus imperialis

<400> 506

Asp Trp Asn Ser Cys Cys Gly Lys Asn Pro Gly Cys Cys Pro Trp
1 5 10 15

<210> 507

<211> 11

<212> PRT

<213> Conus betulinus

<400> 507

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Asn Cys Cys Pro Asp Ser Pro Pro Cys Cys His
1 5 10

<210> 508
<211> 12
<212> PRT
<213> Conus ammiralis

<400> 508
Gly Asn Cys Cys Glu Phe Trp Glu Phe Cys Cys Asp
1 5 10

<210> 509
<211> 9
<212> PRT
<213> Conus dalli

<400> 509
Cys Cys Glu Tyr Trp Lys Leu Cys Cys
1 5

<210> 510
<211> 11
<212> PRT
<213> Conus omaria

<400> 510
Val Cys Cys Gly Tyr Lys Phe Phe Cys Cys Arg
1 5 10

<210> 511
<211> 11
<212> PRT
<213> Conus aulicus

<400> 511
Phe Cys Cys Pro Val Ile Arg Tyr Cys Cys Trp
1 5 10

<210> 512
<211> 11
<212> PRT
<213> Conus aulicus

<400> 512
Phe Cys Cys Pro Phe Ile Arg Tyr Cys Cys Trp
1 5 10

<210> 513
<211> 10
<212> PRT
<213> Conus aulicus

<400> 513
Cys Cys Pro Met Ile Tyr Trp Cys Cys Ser
1 5 10

<210> 514
<211> 10
<212> PRT
<213> Conus aulicus

<400> 514
Cys Cys Pro Glu Ile Tyr Trp Cys Cys Ser
1 5 10

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<210> 515
 <211> 10
 <212> PRT
 <213> *Conus nobilis*

<400> 515
 Ile Cys Cys Pro Ile Ile Leu Trp Cys Cys
 1 5 10

<210> 516
 <211> 9
 <212> PRT
 <213> *Conus ammiralis*

<400> 516
 Cys Cys Pro Pro Val Ile Trp Cys Cys
 1 5

<210> 517
 <211> 11
 <212> PRT
 <213> *Conus textile*

<400> 517
 Cys Cys Gln Thr Phe Tyr Trp Cys Cys Val Gln
 1 5 10

<210> 518
 <211> 13
 <212> PRT
 <213> *Conus aulicus*

<400> 518
 Trp Asn Asn Tyr Cys Cys Thr Asn Glu Leu Trp Cys Cys
 1 5 10

<210> 519
 <211> 13
 <212> PRT
 <213> *Conus gloriamaris*

<400> 519
 Leu Cys Cys Val Thr Glu Asp Trp Cys Cys Glu Trp Trp
 1 5 10

<210> 520
 <211> 11
 <212> PRT
 <213> *Conus gloriamaris*

<400> 520
 Val Cys Cys Arg Pro Val Gln Asp Cys Cys Ser
 1 5 10

<210> 521
 <211> 13
 <212> PRT
 <213> *Conus dalli*

<400> 521
 Pro Val Asn Cys Cys Pro Ile Asp Gln Ser Cys Cys Ser
 1 5 10

<210> 522

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<211> 17
 <212> PRT
 <213> Conus spurius

<400> 522
 Gly Asn Ile His Cys Cys Thr Lys Tyr Gln Pro Cys Cys Ser Ser Pro
 1 5 10 15

Ser

<210> 523
 <211> 12
 <212> PRT
 <213> Conus textile

<400> 523
 Glx Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys
 1 5 10

<210> 524
 <211> 11
 <212> PRT
 <213> Conus bandanus

<400> 524
 Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys
 1 5 10

<210> 525
 <211> 13
 <212> PRT
 <213> Conus pennaceus

<400> 525
 Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg
 1 5 10

<210> 526
 <211> 13
 <212> PRT
 <213> Conus pennaceus

<400> 526
 Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Ser
 1 5 10

<210> 527
 <211> 12
 <212> PRT
 <213> Conus pennaceus

<400> 527
 Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys
 1 5 10

<210> 528
 <211> 12
 <212> PRT
 <213> Conus episcopatus

<400> 528
 Ser Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys
 1 5 10

<210> 529

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<213> Conus stercusmuscarum

<220>

<221> PEPTIDE

<222> (1)..(8)

<223> Xaa is hydroxy-Pro

<400> 542

Gly Cys Xaa Trp Gln Pro Val Cys
1 5

<210> 543

<211> 11

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(11)

<223> Xaa is hydroxy-Pro

<400> 543

Glx Tyr Gly Cys Xaa Xaa Gly Leu Trp Cys His
1 5 10

<210> 544

<211> 10

<212> PRT

<213> Conus arenatus

<400> 544

Ala Ser Gly Cys Pro Trp Arg Pro Trp Cys
1 5 10

<210> 545

<211> 11

<212> PRT

<213> Conus arenatus

<400> 545

Glx Tyr Gly Cys Pro Val Gly Leu Trp Cys Asp
1 5 10

<210> 546

<211> 9

<212> PRT

<213> Conus arenatus

<400> 546

Ser Gly Cys Pro Trp Gln Pro Trp Cys
1 5

<210> 547

<211> 9

<212> PRT

<213> Conus arenatus

<400> 547

Ser Gly Cys Pro Trp His Pro Trp Cys
1 5

<210> 548

<211> 30

<212> PRT

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<220>

<222> (1) .. (30)

<400> 548

Thr Val Gly Arg Xaa Xaa Tyr Cys Asp Arg Xaa Ser Gly Gly
20 25 30

<211>	25
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<213> Conus purpurascens

Gly Cys Cys Gly Ser Tyr Pro Asn Ala Ala Cys His Pro Cys Gly Cys
1 5 10 15

<211> 23

<213> Conus purpurascens

Glu Gly Cys Cys Ser Asn Pro Ala Cys His Pro Cys Gly Cys Lys Asp
1 5 10 15

<210> 551

<212> PRT

<400> 551

Val	Val	Thr	Glu	Ala	Cys	Glu	Glu	Ser	Cys	Glu	Glu	Glu	Glu	Lys	His
1				5					10					15	

Cys Cys His Val Asn Asn Gly Val Pro Ser Cys Ala Val Ile Cys Trp
20 25 30

<211> 32

<213> Conus arenatus

Ile Val Thr Glu Ala Cys Glu Glu Ser Cys Glu Asp Glu Glu Lys His
1 5 10 15

Cys Cys His Val Asn Asn Gly Val Pro Ser Cys Ala Val Ile Cys Trp
20 25 30

<210> 553

<211> 32

<212> PRT

<213> Conus arenatus

<400> 553
 Ile Val Thr Glu Ala Cys Glu Glu His Cys Glu Asp Glu Glu Gln Phe
 1 5 10 15

Cys Cys Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala Pro Val Cys Phe
 20 25 30

<210> 554
 <211> 32
 <212> PRT
 <213> Conus arenatus

<400> 554
 Val Val Thr Gly Ala Cys Glu Glu His Cys Glu Asp Glu Glu Lys His
 1 5 10 15

Cys Cys Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala Arg Leu Cys Leu
 20 25 30

<210> 555
 <211> 32
 <212> PRT
 <213> Conus distans

<400> 555
 Asn Val Asp Gln Glu Cys Ile Asp Ala Cys Gln Leu Glu Asp Lys Asn
 1 5 10 15

Cys Cys Gly Arg Thr Asp Gly Glu Pro Arg Cys Ala Lys Ile Cys Leu
 20 25 30

<210> 556
 <211> 32
 <212> PRT
 <213> Conus distans

<400> 556
 Glu Thr Asp Gln Glu Cys Ile Asp Ile Cys Lys Gln Glu Asp Lys Lys
 1 5 10 15

Cys Cys Gly Arg Ser Asn Gly Glu Pro Thr Cys Ala Lys Ile Cys Leu
 20 25 30

<210> 557
 <211> 32
 <212> PRT
 <213> Conus distans

<400> 557
 Glu Thr Asp Gln Glu Cys Ile Asp Thr Cys Glu Gln Glu Asp Lys Lys
 1 5 10 15

Cys Cys Gly Arg Thr Asn Gly Glu Pro Val Cys Ala Lys Ile Cys Phe
 20 25 30

<210> 558
 <211> 37
 <212> PRT
 <213> Conus purpurascens

<400> 558
 Pro Lys Thr Glu Ala Cys Glu Glu Val Cys Glu Leu Glu Glu Lys His
 1 5 10 15

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Cys Cys Cys Ile Arg Ser Asp Gly Pro Lys Cys Ser Arg Lys Cys Leu
20 25 30

Leu Ser Ile Phe Cys
35

<210> 559
<211> 32
<212> PRT
<213> Conus purpurascens

<400> 559
Val Val Ser Glu Glu Cys Lys Lys Tyr Cys Lys Lys Gln Asn Lys Asn
1 5 10 15

Cys Cys Ser Ser Lys His Glu Glu Pro Arg Cys Ala Lys Ile Cys Phe
20 25 30

<210> 560
<211> 32
<212> PRT
<213> Conus sponsalis

<400> 560
Ala Val Thr Glu Ala Cys Thr Glu Asp Cys Lys Thr Gln Asp Lys Lys
1 5 10 15

Cys Cys Gly Glu Met Asn Gly Gln His Thr Cys Ala Lys Ile Cys Leu
20 25 30

<210> 561
<211> 37
<212> PRT
<213> Conus tulipa

<400> 561
Pro Lys Thr Lys Glu Cys Glu Arg Tyr Cys Glu Leu Glu Glu Lys His
1 5 10 15

Cys Cys-Cys Ile Arg Ser Asn Gly Pro Lys Cys Ser Arg Ile Cys Ile
20 25 30

Phe Lys Phe Trp Cys
35

<210> 562
<211> 36
<212> PRT
<213> Conus tulipa

<400> 562
Pro Lys Thr Arg Glu Cys Glu Met Gln Cys Glu Gln Glu Glu Lys His
1 5 10 15
Cys Cys Arg Val Arg Asp Gly Thr Gly Gln Cys Ala Pro Lys Cys Leu
20 25 30

Gly Ile Asn Trp
35

<210> 563
<211> 9
<212> PRT
<213> Conus geographus

<400> 563

Cys Phe Ile Arg Asn Cys Pro Lys Gly
1 5

<210> 564
<211> 9
<212> PRT
<213> Conus striatus

<400> 564
Cys Ile Ile Arg Asn Cys Pro Arg Gly
1 5

<210> 565
<211> 28
<212> PRT
<213> Conus arenatus

<400> 565
Gly Cys Thr Pro Pro Gly Gly Val Cys Gly Tyr His Gly His Cys Cys
1 5 10 15

Asp Phe Cys Asp Thr Phe Gly Asn Leu Cys Val Ser
20 25

<210> 566
<211> 27
<212> PRT
<213> Conus geographus

<400> 566
Ala Cys Ser Gly Arg Gly Ser Arg Cys Pro Pro Gln Cys Cys Met Gly
1 5 10 15

Leu Thr Cys Gly Arg Glu Tyr Pro Pro Arg Cys
20 25

<210> 567
<211> 31
<212> PRT
<213> Conus characteristicus

<400> 567
Asn Cys Gly Glu Gln Gly Glu Gly Cys Ala Thr Arg Pro Cys Cys Ser
1 5 10 15

Gly Leu Ser Cys Val Gly Ser Arg Pro Gly Gly Leu Cys Gln Tyr
20 25 30

<210> 568
<211> 23
<212> PRT
<213> Conus textile

<400> 568
Asn Cys Pro Tyr Cys Val Val Tyr Cys Cys Pro Pro Ala Tyr Cys Glu
1 5 10 15

Ala Ser Gly Cys Arg Pro Pro
20

<210> 569
<211> 27
<212> PRT
<213> Conus delesstii

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<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 4 is hydroxy-Pro; Xaa at residues 13 and 16 is gam
 m-carboxy-Glu

<400> 569
 Ala Cys Lys Xaa Lys Asn Asn Leu Cys Ala Ile Thr Xaa Met Ala Xaa
 1 5 10 15
 Cys Cys Ser Gly Phe Cys Leu Ile Tyr Arg Cys
 20 25

<210> 570
 <211> 30
 <212> PRT
 <213> Conus lividus

<400> 570
 Ser Cys Gly His Ser Gly Ala Gly Cys Tyr Thr Arg Pro Cys Cys Pro
 1 5 10 15
 Gly Leu His Cys Ser Gly Gly Gln Ala Gly Gly Leu Cys Val
 20 25 30

<210> 571
 <211> 35
 <212> PRT
 <213> Conus lividus

<400> 571
 Asp Cys Gly Glu Ser Gly Gln Gly Cys Tyr Ser Val Arg Pro Cys Cys
 1 5 10 15
 Pro Gly Leu Ile Cys Lys Gly Thr Gly Gly Gly Gly Leu Cys Arg Pro
 20 25 30

Ser Gly Ile
 35

<210> 572
 <211> 31
 <212> PRT
 <213> Conus miliaris
 <400> 572

Cys Thr Pro Pro Gly Gly Leu Cys Tyr His Ala Tyr Pro Cys Cys Ser
 1 5 10 15
 Lys Thr Cys Asn Leu Asp Thr Ser Gln Cys Glu Pro Arg Trp Ser
 20 25 30

<210> 573
 <211> 36
 <212> PRT
 <213> Conus miles

<400> 573
 Cys Thr Asp Asp Ser Gln Phe Cys Asn Pro Ser Asn His Asp Cys Cys
 1 5 10 15
 Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn Gly Ile Cys Ala Ile Val
 20 25 30

Pro Glu Asn Ser

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<210> 574
<211> 36
<212> PRT
<213> Conus miles
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<400> 574
Cys Thr Glu Asp Ser Gln Phe Cys Asn Pro Ser Asn His Asp Cys Cys
1      5      10      15
Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn Gly Ile Cys Ala Ile Val
20      25      30
Pro Glu Asn Ser
35
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<210> 575
<211> 30
<212> PRT
<213> Conus pulicarius
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<400> 575
Cys Ser Asp Phe Gly Ser Asp Cys Val Pro Ala Thr His Asn Cys Cys
1      5      10      15
Ser Gly Glu Cys Phe Gly Phe Glu Asp Phe Gly Leu Cys Thr
      20      25      30

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<210> 576
<211> 30
<212> PRT
<213> Conus quercinus
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<400> 576
Ala Cys Ser Gln Val Gly Glu Ala Cys Phe Pro Gln Lys Pro Cys Cys
1 5 10 15
Pro Gly Phe Leu Cys Asn His Ile Gly Gly Met Cys His His
20 25 30

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<210> 577
<211> 28
<212> PRT
<213> Conus striatus
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<400> 577
Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
1 5 10 15
Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
20 25

<210>	578
<211>	31
<212>	PRT
<213>	Conus tessulatus

<400> 578
Ser Cys Ala Glu Phe Gly Glu Val Cys Ser Ser Thr Ala Cys Cys Pro
1 5 10 15
Asp Leu Asp Cys Val Glu Ala Tyr Ser Pro Ile Cys Leu Trp Glu
20 25 30

<210> 579
 <211> 27
 <212> PRT
 <213> Conus textile

<400> 579
 Lys Cys Val Glu Gln Trp Lys Tyr Cys Thr Arg Glu Ser Leu Cys Cys
 1 5 10 15
 Ala Gly Leu Cys Leu Phe Ser Phe Cys Ile Leu
 20 25

<210> 580
 <211> 29
 <212> PRT
 <213> Conus textile

<400> 580
 Cys Val Glu Gln Trp Glu Val Cys Gly Ile Ile Leu Phe Ser Ser Ser
 1 5 10 15
 Cys Cys Gly Gln Leu Cys Leu Phe Gly Phe Cys Val Leu
 20 25

<210> 581
 <211> 32
 <212> PRT
 <213> Conus virgo

<400> 581
 Asp Cys Gly Gly Gln Gly Glu Gly Cys Tyr Thr Gln Pro Cys Cys Pro
 1 5 10 15
 Gly Leu Arg Cys Arg Gly Gly Gly Thr Gly Gly Gly Val Cys Gln Leu
 20 25 30

<210> 582
 <211> 33
 <212> PRT
 <213> Conus wittigi

<400> 582
 Phe Gly Ser Phe Ile Pro Cys Ala Arg Leu Gly Glu Pro Cys Thr Ile
 1 5 10 15
 Cys Cys Arg Pro Leu Arg Cys Arg Glu Ser Gly Thr Pro Thr Cys Gln
 20 25 30

Val

<210> 583
 <211> 30
 <212> PRT
 <213> Conus regius

<400> 583
 Thr Cys Leu Glu His Asn Lys Leu Cys Trp Tyr Asp Arg Asp Cys Cys
 1 5 10 15
 Thr Ile Tyr Cys Asn Glu Asn Lys Cys Gly Val Lys Pro Gln
 20 25 30

<210> 584
 <211> 34
 <212> PRT

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<400> 584

Tyr Thr Trp Asn Gly Ser Ser Gly Tyr Cys Lys Arg Val Cys Tyr Leu
20 25 30

<210> 585

<211> 24

<212> PRT

<213> Conus purpurascens

 $\langle 220 \rangle$

<221> PEPTIDE

<222> (1) . . (24)

<223> Xaa is hydroxy-Pro

<400> 585

Gly Xaa Xaa Cys Cys Leu Tyr Gly Ser Cys Arg Xaa Phe Xaa Gly Cys
1 5 10 15

Tyr Asn Ala Leu Cys Cys Arg Lys
20

<210> 586

<211> 24

<212> PRT

<213> Conus purpurascens

<400> 586

His Pro Pro Cys Cys Met Tyr Gly Arg Cys Arg Arg Tyr Pro Gly Cys
1 5 10 15

Ser Ser Ala Ser Cys Cys Gln Gly
20

<210> 587

<211> 36

<212> PRT

<213> Conus consors

<400> 587

Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr Asp
1 5 10 15

Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser Cys Pro Pro
20 25 30

Lys Arg Lys Pro
35

<210> 588

<211> 39

<212> PRT

<213> Conus aurisiacus

<400> 588

Glx Ser Trp Leu Val Pro Ser Thr Ile Thr Thr Cys Cys Gly Tyr Asp
1 5 10 15

Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asn Asn Thr Cys Lys Pro

20 25 30
 Lys Lys Pro Lys Pro Gly Lys
 35
 <210> 589
 <211> 37
 <212> PRT
 <213> Conus consors
 <400> 589
 Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr Asp
 1 5 10 15
 Pro Met Thr Trp Cys Pro Ser Cys Met Cys Thr Tyr Ser Cys Pro His
 20 25 30
 Gln Arg Lys Lys Pro
 35
 <210> 590
 <211> 36
 <212> PRT
 <213> Conus magus
 <400> 590
 Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr Asp
 1 5 10 15
 Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser Cys Pro Pro
 20 25 30
 Lys Gly Lys Pro
 35
 <210> 591
 <211> 38
 <212> PRT
 <213> Conus aurisiacus
 <400> 591
 Glx Lys Trp Leu Val His Ser Lys Ile Thr Tyr Cys Cys Gly Tyr Asn
 1 5 10 15
 Lys Met Asp Met Cys Pro Pro Cys Met Cys Thr Tyr Ser Cys Pro Pro
 20 25 30
 Leu Lys Lys Lys Arg Pro
 35
 <210> 592
 <211> 29
 <212> PRT
 <213> Conus aurisiacus
 <400> 592
 Ala Pro Trp Thr Val Val Thr Ala Thr Thr Asn Cys Cys Gly Ile Thr
 1 5 10 15
 Gly Pro Gly Cys Leu Pro Cys Arg Cys Thr Gln Thr Cys
 20 25
 <210> 593
 <211> 13

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 207260-040

<400> 599

Glx	Asp	Tyr	Cys	Cys	Thr	Ile	Pro	Ser	Cys	Trp	Asp	Arg	Tyr	Lys	Glu
1				5					10					15	

Arg	Cys	Arg	His	Ile	Arg
			20		

<210> 600

<211> 13

<212> PRT

<213> Conus miles

<400> 600

Asp	Tyr	Cys	Cys	His	Arg	Gly	Pro	Cys	Met	Val	Trp	Cys
1				5					10			

<210> 601

<211> 13

<212> PRT

<213> Conus jDedius

<400> 601

Gly	Cys	Cys	Ser	Asp	Pro	Arg	Cys	Arg	Tyr	Arg	Cys	Arg
1				5					10			

<210> 602

<211> 17

<212> PRT

<213> Conus omaria

<400> 602

Gly	Cys	Cys	Ser	His	Pro	Ala	Cys	Asn	Val	Asn	Asn	Pro	His	Ile	Cys
1				5					10					15	

Gly

<210> 603

<211> 17

<212> PRT

<213> Conus omaria

<400> 603

Gly	Cys	Cys	Ser	His	Pro	Ala	Cys	Asn	Val	Asn	Asn	Pro	His	Ile	Cys
1				5					10					15	

Gly

<210> 604

<211> 19

<212> PRT

<213> Conus quercinus

<400> 604

Glx	Gly	Cys	Cys	Ser	Asp	Pro	Ala	Cys	Ala	Val	Ser	Asn	Pro	Asp	Ile
1				5					10					15	

Cys Gly Gly

<210> 605

<211> 17

<212> PRT

<213> Conus bandanus

<400> 605

Pro	Glu	Cys	Cys	Thr	His	Pro	Ala	Cys	His	Val	Ser	His	Pro	Glu	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

<400> 618

Gly Cys Cys Ser Asn Pro Pro Cys Tyr Ala Asn Asn Gln Ala Tyr Cys
 1 5 10 15

Asn

<210> 619

<211> 25

<212> PRT

<213> Conus wittigi

<400> 619

Asp Glu Cys Cys Ala His Pro Ser Cys Trp Lys Ala Glu Asp Leu Ile
 1 5 10 15

Cys Thr Asn Gln Arg Arg Arg Thr Leu
 20 25

<210> 620

<211> 20

<212> PRT

<213> Conus characteristicus

<400> 620

Gly Cys Cys Ala Ile Arg Glu Cys Arg Leu Gln Asn Ala Ala Tyr Cys
 1 5 10 15

Gly Gly Ile Ser
 20

<210> 621

<211> 19

<212> PRT

<213> Conus betulinus

<400> 621

Ser Ala Thr Cys Cys Tyr Tyr Pro Pro Cys Tyr Glu Ala Tyr Pro Glu
 1 5 10 15

Ser Cys Leu

<210> 622

<211> 6

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(6)

<223> Xaa is gamma-carboxy-Glu

<400> 622

Val Tyr Xaa Thr His Pro
 1 5

<210> 623

<211> 14

<212> PRT

<213> Conus striatus

<400> 623

Trp Ser Trp Arg Met Gly Asn Gly Asp Arg Arg Ser Asp Gln
 1 5 10

<210> 624

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<211> 11
 <212> PRT
 <213> Conus quercinus

<400> 624
 Asp Cys Gln Pro Cys Gly His Asn Val Cys Cys
 1 5 10

<210> 625
 <211> 29
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(29)
 <223> Xaa is gamma-carboxy-Glu

<400> 625
 Lys Phe Leu Ser Gly Gly Phe Lys Xaa Ile Val Cys His Arg Tyr Cys
 1 5 10 15

Ala Lys Gly Ile Ala Lys Glu Phe Cys Asn Cys Pro Asp
 20 25

<210> 626
 <211> 6
 <212> PRT
 <213> Conus magus

<400> 626
 Arg Pro Lys Asn Ser Trp
 1 5

<210> 627
 <211> 7
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(7)
 <223> Xaa is hydroxy-Pro

<400> 627
 Ala Arg Xaa Lys Asn Ser Trp
 1 5

<210> 628
 <211> 6
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(6)
 <223> Xaa is hydroxy-Pro

<400> 628
 Arg Xaa Lys Asn Ser Trp
 1 5

<210> 629
 <211> 71
 <212> PRT

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<213> Conus geographus

<400> 629

Cys Cys Pro Ser Ser Lys Glu Asp Ser Leu Asn Cys Ile Glu Thr Met
1 5 10 15

Ala Thr Thr Ala Thr Cys Met Lys Ser Asn Lys Gly Glu Ile Tyr Ser
20 25 30

Tyr Ala Cys Gly Tyr Cys Gly Lys Lys Lys Glu Ser Cys Phe Gly Asp
35 40 45

Lys Lys Pro Val Thr Asp Tyr Gln Cys Gln Thr Arg Asn Ile Pro Asn
50 55 60

Pro Cys Gly Gly Ala Ala Leu
65 70

<210> 630

<211> 65

<212> PRT

<213> Conus geographus

<400> 630

Asp Glu Ser Lys Cys Asp Arg Cys Asn Cys Ala Glu Leu Arg Ser Ser
1 5 10 15

Arg Cys Thr Gln Ala Ile Phe Cys Leu Thr Pro Glu Leu Cys Thr Pro
20 25 30

Ser Ile Ser Cys Pro Thr Gly Glu Cys Arg Cys Thr Lys Phe His Gln
35 40 45

Ser Arg Cys Thr Arg Phe Val Glu Cys Val Pro Asn Lys Cys Arg Asp
50 55 60

Ala
65

<210> 631

<211> 60

<212> PRT

<213> Conus geographus

<400> 631

Asp Asp Ser Tyr Cys Asp Gly Cys Leu Cys Thr Ile Leu Lys Lys Glu
1 5 10 15

Thr Cys Thr Ser Thr Met Ser Cys Arg Gly Thr Cys Arg Lys Glu Trp
20 25 30

Pro Cys Trp Glu Glu Asp Cys Tyr Cys Thr Glu Ile Gln Gly Gly Ala
35 40 45

Cys Val Thr Pro Ser Glu Cys Lys Pro Gly Glu Cys
50 55 60

<210> 632

<211> 43

<212> PRT

<213> Conus radiatus

<400> 632

Gly Cys Val Tyr Glu Gly Ile Glu Tyr Ser Val Gly Glu Thr Tyr Gln
1 5 10 15

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Ala Asp Cys Asn Thr Cys Arg Cys Asp Gly Phe Asp Leu Ala Thr Cys
 20 25 30

Thr Val Ala Gly Cys Thr Gly Phe Gly Pro Glu
 35 40

<210> 633
 <211> 86
 <212> PRT
 <213> Conus striatus

<400> 633
 Ser Gly Pro Ala Asp Cys Cys Arg Met Lys Glu Cys Cys Thr Asp Arg
 1 5 10 15

Val Asn Glu Cys Leu Gln Arg Tyr Ser Gly Arg Glu Asp Lys Phe Val
 20 25 30

Ser Phe Cys Tyr Gln Glu Ala Thr Val Thr Cys Gly Ser Phe Asn Glu
 35 40 45

Ile Val Gly Cys Cys Tyr Gly Tyr Gln Met Cys Met Ile Arg Val Val
 50 55 60

Lys Pro Asn Ser Leu Ser Gly Ala His Glu Ala Cys Lys Thr Val Ser
 65 70 75 80

Cys Gly Asn Pro Cys Ala
 85

<210> 634
 <211> 24
 <212> PRT
 <213> Conus purpurascens

<400> 634
 Asp Cys Cys Gly Val Lys Leu Glu Met Cys His Pro Cys Leu Cys Asp
 1 5 10 15

Asn Ser Cys Lys Asn Tyr Gly Lys
 20

<210> 635
 <211> 36
 <212> PRT
 <213> Conus geographus

<400> 635
 Gly Glu Pro Ile Pro Thr Thr Val Ile Asn Tyr Gly Glu Cys Cys Lys
 1 5 10 15

Asp Pro Ser Cys Trp Val Lys Val Lys Asp Phe Gln Cys Pro Gly Ala
 20 25 30

Ser Pro Pro Asn
 35

<210> 636
 <211> 16
 <212> PRT
 <213> Conus generalis

<400> 636
 Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Val Pro
 1 5 10 15

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<210> 637
 <211> 20
 <212> PRT
 <213> Conus tessulatus

<400> 637
 Asp Gly Cys Pro Pro His Pro Val Pro Gly Met His Lys Cys Met Cys
 1 5 10 15
 Thr Asn Thr Cys
 20

<210> 638
 <211> 84
 <212> PRT
 <213> Conus radiatus

<400> 638
 His Pro Thr Lys Pro Cys Met Tyr Cys Ser Phe Gly Gln Cys Val Gly
 1 5 10 15
 Pro His Ile Cys Cys Gly Pro Thr Gly Cys Glu Met Gly Thr Ala Glu
 20 25 30
 Ala Asn Met Cys Ser Glu Glu Asp Glu Asp Pro Ile Pro Cys Gln Val
 35 40 45
 Phe Gly Ser Asp Cys Ala Leu Asn Asn Pro Asp Asn Ile His Gly His
 50 55 60
 Cys Val Ala Asp Gly Ile Cys Cys Val Asp Asp Thr Cys Thr Thr His
 65 70 75 80
 Leu Gly Cys Leu

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